

## SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: \_\_\_\_\_ Examiner #: \_\_\_\_\_ Date: \_\_\_\_\_  
Art Unit: \_\_\_\_\_ Phone Number 30 \_\_\_\_\_ Serial Number: \_\_\_\_\_  
Mail Box and Bldg/Room Location: \_\_\_\_\_ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

\*\*\*\*\*  
Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers; and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

*\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval  
Reference Librarian  
Biotechnology & Chemical Library  
CM1 1E07 - 703-308-4498  
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\*\*\*\*\*  
STAFF USE ONLYSearcher: JanSearcher Phone #: 4498

Searcher Location: \_\_\_\_\_

Date Searcher Picked Up: 12/2/02Date Completed: 12/2/02

Searcher Prep &amp; Review Time: \_\_\_\_\_

Clerical Prep Time: 10Online Time: 10

## Type of Search

NA Sequence (#) \_\_\_\_\_

AA Sequence (#) ☒

Structure (#) \_\_\_\_\_

Bibliographic \_\_\_\_\_

Litigation \_\_\_\_\_

Fulltext \_\_\_\_\_

Patent Family \_\_\_\_\_

Other \_\_\_\_\_

## Vendors and cost where applicable

STN \_\_\_\_\_

Dialog \_\_\_\_\_

Questel/Orbit \_\_\_\_\_

Dr.Link \_\_\_\_\_

Lexis/Nexis \_\_\_\_\_

Sequence Systems ☒

WWW/Internet \_\_\_\_\_

Other (specify) \_\_\_\_\_

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 2, 2002, 12:54:49 ; Search time 16.7172 Seconds  
(without alignments)  
1742.436 Million cell updates/sec

Title: US-09-895-263-2

Perfect score: 1613

Sequence: 1 MADQCGIEGVEDSAND.....EKKQIPCVSMULTKELYESQ 303

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	751	46.6	277	2	S64710
2	718	44.5	277	2	A55315
3	699	43.3	277	2	UC5410
4	580.5	36.0	212	2	167437
5	377	23.4	503	2	A49429
6	371.5	23.0	454	2	JC7123
7	354.5	22.0	416	2	G02635
8	349.5	21.7	495	2	T20038
9	317	19.7	435	2	A54821
10	305	18.9	452	2	JC6507
11	305	18.9	826	2	T43638
12	284	17.6	536	2	T43633
13	255	15.8	242	2	JC7517
14	250	15.5	642	2	T27021
15	246.5	15.3	488	2	T13851
16	210	13.0	418	2	B57511
17	199.5	12.4	182	2	167436
18	195	12.1	404	2	A42677
19	189.5	11.7	311	2	B56084
20	189.5	11.7	383	2	A56084
21	189	11.7	312	2	B54821
22	189	11.7	402	2	A46495
23	184	11.4	377	2	A57511
24	156.5	9.7	263	2	C56084
25	145.5	9.0	149	2	T43637
26	143.5	8.9	139	2	T43642
27	139	8.6	136	2	I53300
28	117	7.3	394	2	T26968
29	99.5	6.2	282	2	I84621

30	94.5	5.9	603	2	B64444	hypothetical prote
31	94.5	5.9	761	2	B97163	ATP-dependent seri
32	93.5	5.8	612	2	E84809	hypothetical prote
33	93	5.8	1151	2	T04657	hypothetical prote
34	93	5.8	1643	2	T07961	myosin heavy chain
35	91	5.6	1100	1	DD81D1	Rd1 protein - yea
36	89.5	5.5	1553	2	T18502	hypothetical prote
37	89.5	5.5	459	2	J00419	coagulation factor
38	89.5	5.5	857	2	T25465	hypothetical prote
39	87.5	5.4	1314	2	T47331	hypothetical prote
40	87.5	5.4	1358	2	A29360	Sir4 protein - yea
41	86	5.3	222	2	T26944	hypothetical prote
42	86	5.3	1004	2	JC2221	major surface glyc
43	86	5.3	1157	2	H69163	DNA helicase relat
44	85.5	5.3	330	2	T17593	mRNA guanylyltrans
45	85.5	5.3	486	2	A11942	cysteiny1-tRNA syn

## ALIGNMENTS

## RESULT 1

S64710  
Cysteine proteinase (EC 3.4.22.-) CPP32 - Chinese hamster  
C:Species: Crictetus griseus (Chinese hamster)  
C:Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 05-Nov-1999  
C:Accession: S64710; S72395  
R:Wang, X.; Zelenski, N.G.; Yang, J.; Sakai, J.; Brown, M.S.; Goldstein, J.L.  
EMBO J. 15, 1012-1020, 1996  
A:Title: Cleavage of sterol regulatory element binding proteins (SREBPs) by CPP32 dur  
A:Reference number: S64710; M01D:96183185; PMID:8605870  
A:Accession: S64710  
A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-277 <MAN>

A:Cross-references: EMBL:U27463

R:Wang, X.

submitted to the EMBL Data Library, May 1995

A:Reference number: S72395

A:Accession: S72395

A:Molecule type: mRNA

A:Residues: 1-79, 'A', 81-146, 'Y', 148-277 <MAN>

A:Cross-references: EMBL:U27463; NID:91244443; PIDN:AAB01511.1; PID:91244444

C:Keywords: apoptosis; cysteine proteinase; hydrolase

Query Match 46.6%; Score 751; DB 2; Length 277;  
Best local Similarity 52.4%; Pred. No. 2, 5e-57;  
Matches 150; Conservative 46; Mismatches 74; Indels 16; Gaps 3;

QY	18	NEDSVAKPDRSSVPSLFSKKK--KNVTKRSIKTTRDVPYQYNNFEKIGKCIINN	75
DB	4	NETSVDSKSKINEVKTTHSGSKMSDGIYIDS-----SKNDYPMGVCIIINN	52
QY	76	KNTDKVYGMGVNGTDKDAELFKFERSLGFVIVYNDSCAKMQLDKKASEDHNTAA	135
DB	53	KNHKSKGMPFRSGTDVDAKLRETFMNLKYEVANKNDLREVELLMKNASKSDHSRS	112
QY	136	CFPACILSHGEENVYIKGDCVTPPKDLTAHFRGDRCTLLKPKLFTIOACRGELDDAI	195
DB	113	SFVCVILSHGDEGVITGTDGPDIDKLKLTSTYFRGDRCSLIGKPKLFTIOACRGTELDCGI	172
QY	196	QAQSGPINTDANPRKRIPEADFLFAYSTVPGYYSRSGSGSFVQALCSILEHGKE	255
DB	173	ETDSGEDDMTCQ--KIPEADFLFAYSTAPGYYSWRNRDGSWFTQSLCSMLKLYAHK	
QY	256	LEIMQITRVNDVAVRHFEESODPHREKKQIPCVSMULTKELYF	301
DB	230	LEPMHILTRVNRKVAPEFSFSDSTPHAKQIPCVSMULTKELYF	275

RESULT 2  
A55315  
cysteine proteinase (EC 3.4.22.-) CPP32 precursor - human

N:Alternate names: cysteine proteinase CPP32  
C:Species: Homo sapiens (man)  
C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 01-Dec-2000  
C:Accession: A55315, S58699; I39005  
R:Bernardes-Alnemri, T.; Litwack, G.; Alnemri, E.S.  
J. Biol. Chem. 269, 30761-30764, 1994  
A:Title: CPP32, a novel human apoptotic protein with homology to *Caenorhabditis elegans*  
A:Reference number: A55315; MUID:95074098; PMID:7983002  
A:Accession: A55315  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-277 <FEER>  
A:Cross-references: GB:O13737; NID:9561665; PIDN:AA65015.1; PID:9561666  
R:Nicholson, D.W.; Ali, A.; Thornberry, N.A.; Viallancourt, J.P.; Ding, C.K.; Gallant, D.  
Yu, V.L.; Miller, D.K.  
Nature 376, 37-43, 1995  
A:Title: Identification and inhibition of the ICE/CED-3 protease necessary for mammalian  
A:Reference number: S58699; MUID:95319529; PMID:7596430  
A:Accession: S58699  
A:Molecule type: protein  
A:Residues: 29-46;176-189,'E',191-193 <NIC>  
R:Cellari, M.; Qian, L.T.; O'Rourke, K.; Desnoyers, S.; Zeng, Z.; Beidler, D.R.; Poitrier  
Tew 81, 801-809, 1995  
A:Title: Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitible protease  
A:Reference number: A56924; MUID:95292347; PMID:7774019  
A:Accession: I39005  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-189,'E',191-277 <RES>  
A:Cross-references: EMBL:U06944; NID:9857568; PIDN:AAA74929.1; PID:9857569  
C:Keywords: apoptosis; cysteine proteinase; hydrolase; lymphocyte

[illegible]

C;Comment: This protein is involved in the apoptosis of dorsal root ganglia neurons.

[illegible]

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RESULT 4
167437
cysteine proteinase (EC 3.4.22.-) P32 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C:Accession: I67437
R:Flaws: J.A.; Kuzv; Tirovich, A.M.; Desanti, A.; Tilly, K.I.; Hirschfield, A.N.;
Endocrinology 136, 5042-5053, 1995
A>Title: Interleukin-1-beta-converting enzyme-related proteases (IRPs) and mammalian
nucleo cells of the ovarian follicle.
A:Reference number: I53300; MUID:96042508; PMID:7588240
A:Accession: I67437
A>Status: preliminary: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-212 <RES>
C:Keywords: cysteine proteinase; hydrolase

Query Match          36.0%   Score 580.5; DB 2; Length 212;
Best Local Similarity 52.7%; Pred. No. 9.8e-43;
Matches 109; Conservative 37; Mismatches 58; Indels 3; Gaps 1;

QY      60 YNNFEKLGKCIIINNKNFKDKVTGCMGYANGTIDKADEALFCKFRSLGFPIVITYNDSCAKM 119
        |:|:::| |:::| |:::| ||||| ||||| :| :|:::| | :| :|
DY      8 YKM DYPEMGCLTIINNNKFHSTGMASARNGDVDAANLRFFPMALKYEVRNKNNDLTREI    67

QB      120 QDLKKRASSEDHTNAACFACILLSHGEBENVITGKDGTPIKDLTAHFGRDCKTLLEPRK 179
        ::|:||||:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DY      68 MELSDVSKEEDSKSRSSFVCYLISHGEDEVIFGTNGPVDLKLKTTFEFGDYCRSLTGPK 127

QB      180 LFTIOARGTELDALIQADSPINDTPANRPYRKIPVEADFPAISTVGYYSMKSPGGGS 239
        ||||| ||||| ||||| ||||| :| :| :| :| :| :| :| :| :| :|
DY      128 LFTIOARGTELDGLETDSAGDDVAQC--KRVEADFLAVASSAGYYSWNRSGS 184

QY      240 MFVOALCSILEEHGKELEIMOLTRVN 266
        ||:|:||:|:|:|:| ||| |||||
DY      185 WFIQSUCAMKLIVAHKLEPFHIHLRVN 211

```

Cell 75, 641-652, 1993  
A:Title: The C. elegans cell death gene ced-3 encodes a protein similar to mammalian int  
A:Reference number: A49429; MUID:94061982; PMID:8242740  
A:Accession: A49429  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-503 <YUA>  
A:Cross-references: GB:I29052; NID:g6503232; PIDN:AAA27982.2; PID:g6503233  
A:Note: sequence extracted from NCBI backbone (NCBIN:139825, NCBIPI:139826)  
A:Accession: T37312  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-417/R, 419-503 <YU>  
A:Cross-references: EMBL:L29052; PIDN:AAA27982.1  
C:Genetics:  
A:Gene: ced-3  
A:Introns: 45/3; 94/2; 179/1; 289/3; 361/1; 403/3; 483/3  
  
Query Match 23.4%; Score 377; DB 2; Length 503;  
Best Local Similarity 31.9%; Pred. No. 1,1e-24;  
Matches 106; Conservative 49; Mismatches 117; Indels 60; Gaps 14;  
  
QY 6 GCIEOGVEDSANEDSVADKPRDSFVSLFSKKKN-VTKRSIKTTRDVPVYNNNF 64  
187 GC-SLIGSSSRNRSFKA-----SGPTQYIFHEEDMNFVDAPTISRVEDKTRM--NF 238  
DB 65 EK-LGKCIINNNKFDKVTGCVNGTGDKAELFKFRSIFDVIYVNDSCAMODL 123  
239 SSPRGMCIIINNEHEQ---MPTNNGTKADKNDLNLNFRMGVITYICNDNLGRMLTI 295  
QY 124 KK-ASEDHTNAACFACILSLSHGEBNVIYKDGVT---PIKDLTAHFGDRCKTLEKP 178  
296 RDKFKHSHGSAITL-VILSHGEBNVIIGVDPISTHEIYDLNANAPR---LANKP 350  
DB 179 KLEFIOACRGTELDADIAQADSGPINDT-DANPRY----- 211  
351 KIVVQACRGERRNGF---PVLDSDGVPAFLRRGMNDNRDGLFNFELGCVRPQVOY 405  
QY 212 --KIPVADFLFAYSTVPGYYSRSPGSGFWQALCSILEBHGKLEIMQILTRVNDRV 269  
406 WRKRPQADILIAATTAQVYSRNSRSGSFIOACVEFSTHAKMDVVELLTVNNKV 465  
DB 270 ARHESQSDDPHFHEKKQIPCVSMLTKELYE 301  
466 ACGFOTSGS---NILKOMPEMTSRLKKPFY 494  
  
RESULT 6  
JC7123  
C:Species: long chain - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 23-Mar-2001  
C:Accession: JC7123  
R:Fujita, E.; Jinbo, A.; Matuzaki, H.; Konishi, H.; Kikawa, U.; Momoi, T.  
Biochem. Biophys. Res. Commun. 264, 550-555, 1999  
A:Title: Akt phosphorylation site found in human caspase-9 is absent in mouse caspase-9  
A:Reference number: JC7123; MUID:20001956; PMID:10529400  
A:Accession: JC7123  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-454 <FUJ>  
A:Cross-references: DDBJ:AB019600; NID:g6440941; PID:g6440942  
  
Query Match 23.0%; Score 371.5; DB 2; Length 454;  
Best Local Similarity 32.8%; Pred. No. 3e-24;  
Matches 90; Conservative 43; Mismatches 96; Indels 45; Gaps 6;  
  
QY 60 YNNMPEKLGKCIINNNKFDKVTGCVNGTGDKAELFKFRSIFDVIYVNDSCAKM 119  
191 YTLSDPGCHLITNNVFCSSGGLGTGSDIDKLEHRRFLRMFEVANKDLTAKKM 250  
QY 120 QDLKKASEEDHTNAACFACILSLSHGEE-----NVIYKDGVT-PIKDLTAHFGDRCK 171

DB 251 VTALNEMAHNRHRAIDCFVYVILSHGQASHLQFPGAVYGTGCSYSEKIYNIENGSGC 310  
QY 172 KTLLEKPKLFTIOACRGTELD-----AIOADSGPINDTDANPR----- 210  
DB 311 PSLGKPKLFTIOACRGTELD-----AIOADSGPINDTDANPR----- 210  
QY 211 KIPVADFLFAYSTVPGYYSRSPGSGFWQALCSILEBHGKLEIMQILTRVNDRV 270  
DB 371 SSLPPSDILVSYSTFPGVSWDRKSGSWYETEDGILFQWARSBDLQSLLRVANAAS 430  
QY 271 RHESQSDDPHFHEK---KQIPCVSMLTKELYE 301  
DB 431 -----EKGYTKQIPGCENFLKKLFF 451  
  
RESULT 7  
G02635  
ICE-LAP6 - human  
C:Species: Homo sapiens (man)  
C:Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 05-Nov-1999  
C:Accession: G02635  
R:Duan, H.; Orth, K.; Chinnaiyan, A.M.; Polier, G.C.; Froelich, C.J.; He, W.W.; Dixi  
submitted to the EMBL data library, April 1996  
A:Reference number: H01513  
A:Accession: G02635  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-416 <DUA>  
A:Cross-references: EMBL:U56390; NID:g1336026; PIDN:AC50640.1; PID:g1336027  
  
Query Match 22.0%; Score 354.5; DB 2; Length 416;  
Best Local Similarity 32.1%; Pred. No. 7.9e-23;  
Matches 88; Conservative 41; Mismatches 100; Indels 45; Gaps 6;  
  
QY 60 YNNMPEKLGKCIINNNKFDKVTGCVNGTGDKAELFKFRSIFDVIYVNDSCAKM 119  
DB 153 YLSMEPCGHCLITNNVFCSSGGLGTGSDIDKLEHRRFLRMFEVANKDLTAKKM 212  
QY 120 QDLKKASEEDHTNAACFACILSLSHGEE-----NVIYKDGVT-PIKDLTAHFGDRCK 171  
DB 213 VIALLERARQDHGALDCCVYVILSHGQASHLQFPGAVYGTGCGPVSVEKIYNIENGSGC 272  
QY 172 KTLLEKPKLFTIOACRGTELDADIAQADSGPINDT-DANPRY----- 212  
DB 273 PSLGKPKLFTIOACRGTELDADIAQADSGPINDT-DANPRY----- 212  
QY 213 --IPVADFLFAYSTVPGYYSRSPGSGFWQALCSILEBHGKLEIMQILTRVNDRV 270  
DB 333 SSLPPSDILVSYSTFPGVSWDRKSGSWYETEDGILFQWARSBDLQSLLRVANAAS 392  
QY 271 RHESQSDDPHFHEK---KQIPCVSMLTKELYE 301  
DB 393 -----VKGYTKQIPGCENFLKKLFF 413  
  
RESULT 8  
T20038  
hypochemical protein C48D1.2 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T20038  
R:Burton, J.  
submitted to the EMBL data library, October 1996  
A:Reference number: Z19214  
A:Accession: T20038  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-495 <WIL>  
A:Cross-references: EMBL:Z81049; PIDN:CAB02848.1; GSPDB:GN00022; CESP:C48D1.2  
A:Experimental source: clone C48D1  
C:Genetics:  
A:Gene: CESP:C48D1.2  
A:Map position: 4



A:introns: 44/3; 93/2; 178/1; 288/3; 360/1; 402/3; 466/1

## Query Match

Best Local Similarity 21.7%; Score 349.5; DB 2; Length 495;

Matches 97; Conservative 48; Mismatches 87; Indels 81; Gaps 13;

QY 22 VDAKPRSSFPVPLFSKKKKNTVMSIKTRDRY-----PT-----YQYNNNF----- 64  
 DB 170 VNAFPQSPSSANSFT-----GCSSLSGSSSRNNSFKASPSPTQYIHEDMNFVADPTIS 225  
 QY 65 ----EKL-----GKCIINNNKNDKVTGNGVNRGTDKDAEALFKCFRSLGFDVIYV 111  
 DB 226 RVFDEKTYRNFSPPRGMCIIINHEHEQ---MPTNRGTADNDNLNLRGMYTICK 282  
 QY 112 NDCSCAKMODLLK-ASEEDHTNAACFACILSHGEBNVIYKDGVT---PIKDLTAHF 166  
 DB 283 DMTGKMLTTITDFAKHSHGDSAIL--VILSHGEBNVIIGVDIPITSTHEYIDLNNA 340  
 QY 167 RGDRCKTLEKPLFTFOACRGTELDADIAQDSGPINDT--DAMPY----- 211  
 DB 341 NMPR---LANKPRIVVOACRGERRNGF---PVLDSVGVPAFLRGMDNRDGPLN 392  
 QY 212 -----KIPVEADFLFAYSTVGYSWRSPGRGSMFVOALCSILEHGKELE 257  
 DB 393 FLGCVRPQVOQVWRKKRPSQADILIAATTAQYVSMNSARGSFIOAVCEVSTHAKMD 452  
 QY 258 IMQILTRVNDRA 270  
 DB 453 VVELLTENVKKYA 465

## RESULT 9

A:4821

apoptosis regulator ICH-1, stimulatory form L - human

C:Species: Homo sapiens (man)

C:Date: 28-Apr-1995 #sequence\_revision 28-Apr-1995 #text\_change 17-Mar-1999

C:Accession: A54821

R:Wang, L.; Miura, M.; Bergeron, L.; Zhu, H.; Yuan, J.

Cell 78; 739-750, 1994

A:Title: Ich-1, an Ice/Ced-3-related gene, encodes both positive and negative regulators

A:Reference number: A54821; MUID:94373811; PMID:8087842

A:Accession: A54821

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-435 <MAN>

A:Cross-references: GB:U13021; NID:9537291; PID:9537292

C:Keywords: alternative splicing; apoptosis

## Query Match

Best Local Similarity 19.7%; Score 317; DB 2; Length 435;

Matches 75; Conservative 52; Mismatches 112; Indels 16; Gaps 6;

QY 60 YNNNEKLGKCIINNNKNDKVTGNGVNRGTDKDAEALFKCFRSLGFDVIYVNDSCAKM 119  
 DB 175 YRLQSRPRGLALVLSVHTGKELEFRSGGDVDTLTFLKLLIDVHVLCDQTAQEM 234  
 QY 130 QDLKASEEDHTNAACFACI--LSHGEBNVIYKDG-VTPIKDLTAHFRGDRCKTLE 176  
 DB 235 QEKLNFAQLP-AHRYTDSICVALLSHGEGALIVGDGKLLQGEVQLDNANCSLON 293  
 QY 177 KKKLFFIOACRGTELDADIAQDSGP-----INDTAN---PRKIPEADFLFAYST 225  
 DB 294 KKKMFIOACRGTELDADIAQDSGP-----INDTAN---PRKIPEADFLFAYST 225  
 QY 226 VGGYSWRSPGRGSMFVOALCSILEHGKELEIMQILTRVNDRAHNFESQSDPPHNEK 285  
 DB 354 LKGTAAAMRTKGSWTIEALQVFSERACDMYADMLVKN-ALIKDRGAYAGTEFHNC 412  
 QY 286 KQIPCVSMLTRKELY 300  
 DB 413 KEMSEYCSFLCRHLY 427

## RESULT 10

JC6507

caspase-2 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 21-Jul-2000

C:Accession: JC6507

R:Sato, N.; Milligan, C.E.; Uchiyama, Y.; Oppenheim, R.W.

Gene 202, 127-132, 1997

A:Title: Cloning and expression of the cDNA encoding rat caspase-2.

A:Reference number: JC6507; MUID:98087427; PMID:9427555

A:Accession: JC6507

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-452 <SAT>

A:Cross-references: GB:07933; NID:92769705; PIDN:AAB96379.1; PID:92769706

## Query Match

Best Local Similarity 18.9%; Score 305; DB 2; Length 452;

Matches 76; Conservative 55; Mismatches 110; Indels 18; Gaps 7;

QY 58 YQ--YNNNEKLGKCIINNNKNDKVTGNGVNRGTDKDAEALFKCFRSLGFDVIYVNDSC 115  
 DB 188 YQLAAYRQSPRGALVMSVHTGKDLFRSGGDVDTLTFLKLLGYNVHLYDQT 247  
 QY 116 CAKMODLLKASEEDHTNAACFACI--LSHGEBNVIYKDG-VTPIKDLTAHFRGDRCK 172  
 DB 248 AOEWQEKLNFAQLP-AHRYTDSICVALLSHGEGALIVGDGKLLQGEVFLRPNANCP 306  
 QY 173 TLEKPLFTFOACRGTELDADIA-----QADSGPINDTANP---RYKIPEADFLF 221  
 DB 307 SLQNKPRMFFIOACRGTELDADIA-----QADSGPINDTANP---RYKIPEADFLF 221  
 QY 222 AYSTVPGYSWRSPGRGSMFVOALCSILEHGKELEIMQILTRVNDRAHNFESQSDPPH 281  
 DB 367 GYACIKNNAAMRTKGSWTIEALQVFSERACDMYADMLVKN-ALIKDRGAYAGTE 425  
 QY 282 FHEKKQIPCVSMLTRKELY 300  
 DB 426 FHRCKEMSEYCSFLCRHLY 444

## RESULT 11

T43638

caspase-related proteinase 2A (EC 3.4.22.-) - Caenorhabditis elegans

N:Contains: caspase 2B

C:Species: Caenorhabditis elegans

C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jul-2000

C:Accession: T43638; T43639

R:Shaham, S.

J. Biol. Chem. 273, 35109-35117, 1998

A:Title: Identification of multiple Caenorhabditis elegans caspases and their potent

A:Reference number: 222587; MUID:99074291; PMID:9657046

A:Accession: T43638

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-826 <SHA>

A:Cross-references: EMBL:AF088288; NID:94063373; PIDN:AAC98295.1; PID:94063374

A:Accession: T43639

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 564-826 <SH2>

A:Cross-references: EMBL:AF088289; NID:94063375; PIDN:AAC98296.1; PID:94063376

A:Gene: csp-2

A:Map position: 4

C:Keywords: cysteine proteinase; hydrolase

## Query Match

Best Local Similarity 18.9%; Score 305; DB 2; Length 826;

Matches 79; Conservative 53; Mismatches 96; Indels 36; Gaps 8;

QY 57 TYOYNNNEKLGKCIINNNKNDKVTGNGVNRGTDKDAEALFKCFRSLGFDVIYVNDSC 116

Db 578 TRKRNRRSSKRAIINNVY---CGMEKRIGSDKDKKLSKLFERLQYSTYDNLS 634

QY 117 AKMODLKKASEEDHTNACACILLSHGSENNVYIGDGYPIIDL-----TAHFQCD 169

Db 635 SEILETVROFTQSHNGSLIIT--IMSHGDGLLYGVGV--PVOMLIDIMLCTA----- 686

QY 170 RCTYLEKPLFTFOACRGTELDADIAQDSGPIINDTANPRY-----KIP-----VEA 217

Db 687 ---SLAKPRPMKVCRCGRIDRAVRCDFIDNFPDRFPFQPMKSKFSSHOTSSQA 743

QY 218 DFLFAYSTVPGYYSWRSPGRGSMFVQALCSILEHGELEIMQILTRVNDVRAHFESQS 277

Db 744 DLVYFSTSPGFLSFREDTGTWYIQELRYVLIENAKOTHLADILMETNRVREKYE-- 801

QY 278 DDPHFHEKKQIPCVVSMULTKELYF 301

Db 802 -DKVYIVCKQAPFEMSRPTKOLF 824

## RESULT 12

T43633

caspace-related proteinase 1A (EC 3.4.22.-) - Caenorhabditis elegans

N:Contains: caspase 1B

C:Species: Caenorhabditis elegans

C>Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jul-2000

C:Accession: T43633; T43636

R:Shaham, S.

J. Biol. Chem. 273, 35109-35117, 1998

A:Title: Identification of multiple Caenorhabditis elegans caspases and their potential

A:Reference number: 222587, PMID:99074291, PMID:9857046

A:Accession: T43633

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-536 <SHA>

A:Cross-references: EMBL:AF088285; NID:94063367; PIDN:AC98292.1; PID:94063368

A:Accession: T43636

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 269-536 <SHA>

A:Cross-references: EMBL:AF088286; NID:94063369; PIDN:AC98293.1; PID:94063370

C:Genetics:

A:Gene: csp-1

A:Map position: 2

C:Function:

A:Description: probably acts in proteolytic cascades to regulate processes such as progl

C:Keywords: cysteine proteinase; hydrolase

Query Match 17.6%; Score 284; DB 2; Length 536;

Best Local Similarity 27.9%; Pred. No. 1,4e-16;

Matches 74; Conservative 50; Mismatches 109; Indels 32; Gaps 7;

QY 58 YQYNNFEKLGKCIITNNKNDKVTGMGVRNGTDKDALELFKCRSLGFDVIVYNDSCA 117

Db 283 YCEMNSNPCTVLTLSNENF---KNMERVGTGKODEVNLTKLFQKQYTVICKRNLAE 339

QY 118 KMDDLKKAASEEDHTNACACILLSHGSENNVYIGD---GYTPIKDLTAHFRGRCK 172

Db 340 SMLEAIKEFEMAHDS--ILFLSHGDGSGVFGIDDMVNNMEVSTYLAH-----Q 392

QY 173 TLEKPLFTFOACRGTELDADIAQDSGPIINDTANPRYK-----PVEAD 218

Db 393 NLLKPKWVAVSACRGKLMGVAVDGLPALEDCAPISEFWNLMMSRIMPCTSLNAD 452

QY 219 FLFAYSTVPGYYSWRSPGRGSMFVQALCSILEHGELEIMQILTRVNDVRAHFESQD 278

Db 453 VILSFTSDGFTSRDEAGTWTIKSKVFNKSKTMHLLDILTEGRNVVTKYENVQG 512

QY 279 DDPHFHEKKQIPCVVSMULTKELYFSQ 303

Db 513 NVVL---KQAPFELISRLTKQMHFSR 534

## RESULT 13

JC7517

Caspase-14/a - human

C:Species: Homo sapiens (man)

C>Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001

C:Accession: JC7517

R:Rechart, L.; Ban, J.; Fischer, H.; Tschachler, E.

Biochem. Biophys. Res. Commun. 277, 655-659, 2000

A:Title: Caspase-14: Analysis of gene structure and mRNA expression during keratinocy

A:Reference number: JC7517; MUID:20517231; PMID:11062009

A:Contents: Epidermal keratinocytes

A:Accession: JC7517

A:Molecule type: mRNA

A:Residues: 1-242 <ECC>

A:Cross-references: GB:AF097874

C:Comment: This enzyme accumulates during keratinocyte differentiation and is activat

C:Genetics:

A:Gene: casp-14/a

A:Map position: 19p13.1

A:Introns: 9/3; 59/3; 135/1; 174/1; 208/3

C:Keywords: differentiation

Query Match 15.8%; Score 255; DB 2; Length 242;

Best Local Similarity 28.0%; Pred. No. 1.6e-14;

Matches 69; Conservative 46; Mismatches 111; Indels 20; Gaps 5;

QY 59 QYNNFEKLGKCIITNNKNDKVTGMGVRNGTDKDALELFKCRSLGFDVIVYNDSCA 118

Db 11 KYDMGATLALILCVTK-----AREGSEEDLDALEHMFQRLRFESTMKRDPATAQ 60

QY 119 MODLLK---ASEEDHTNACACILLSHGSENNVYIGD---GYTPIKDLTAHFRGRCKTL 174

Db 61 FOELEKFOQALIDREDPVSACFVVLMAHGRGFLKGEDEVKLENEALNNKNCAL 120

QY 175 LEKPLFTFOACRGTELDADIAQDSGPIINDTANPRYKIPVADFLFAYSTVPGYYSWR 234

Db 121 RAKRVYITIQACRGGRQRPGEVSGDELYMTKDSPTPTTDLAHVSTEGYIAHYH 180

QY 235 PGRGSMFVQALCSILEHGELEIMQILTRVNDVRAHFESQSDDPHFHEKKQIPCVSM 294

Db 181 DQKSGCFIOTLVDPYTK--RKGHILELLETVYRMAEALVQEG---KARKTNPETQST 234

QY 295 LTKELY 300

Db 235 LKRLY 240

## RESULT 14

T27021

hypothetical protein Y48E1B.13 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C:Accession: T27021

R:McMurray, A.

submitted to the EMBL Data Library, March 1997

A:Reference number: 220299

A:Accession: T27021

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-642 <WIL>

A:Cross-references: EMBL:Z93393; PIDN:CA807698.1; GSPDB:GN00020; CESP:Y48E1B.13

A:Experimental source: clone Y48E1B

C:Genetics:

A:Gene: CESP:Y48E1B.13

A:Map position: 2

A:Introns: 79/3; 122/3; 239/2; 286/3; 333/1; 417/3; 487/1; 589/1; 609/3

Query Match 15.5%; Score 250; DB 2; Length 642;

Best Local Similarity 28.7%; Pred. No. 1.5e-13;

Matches 64; Conservative 41; Mismatches 94; Indels 24; Gaps 6;

QY 58 YQYNNFEKLGKCIITNNKNDKVTGMGVRNGTDKDALELFKCRSLGFDVIVYNDSCA 117

Db 361 YCEMNSNPCTVLTLSNENF---KNMERVGTGKODEVNLTKLFQKQYTVICKRNLAE 417



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 2, 2002, 12:54:49 ; Search time 10.4483 Seconds

(without alignments)  
1202.814 Million cell updates/sec

Title: US-09-895-263-2

Perfect score: 1613  
Sequence: 1 MADDOGCIIEEDGVEDSANED.....EKKQIPCVVSMILTKELYSQ 303

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 segs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the total of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Length	ID	Description
1	1606	99.6	303 1	ICE7_HUMAN
2	1394	86.4	303 1	ICE7_MESAU
3	1346	83.4	303 1	ICE7_MOUSE
4	744	46.1	277 1	ICE3_CRITO
5	718	44.5	277 1	ICE3_HUMAN
6	716	44.4	277 1	ICE3_RAT
7	703	43.6	277 1	ICE3_MOUSE
8	662.5	41.1	282 1	ICE3_XENLA
9	552	34.2	299 1	ICE1_SPOFR
10	539	33.4	339 1	ICE1_DROME
11	532.5	33.0	323 1	ICE1_DROME
12	483.5	30.0	276 1	ICE6_MOUSE
13	466	28.9	293 1	ICE6_HUMAN
14	425.5	26.4	479 1	ICE8_HUMAN
15	395	24.5	521 1	ICEA_HUMAN
16	379	23.5	496 1	CEB3_CAEVU
17	377	23.4	503 1	CEB3_CAEVU
18	349.5	21.7	416 1	CEB3_CAEVU
19	343	21.3	424 1	ICE2_HUMAN
20	317	19.7	435 1	ICE2_HUMAN
21	308	19.1	435 1	ICE2_MOUSE
22	255	15.8	242 1	ICEE_HUMAN
23	251.5	15.6	257 1	ICEE_MOUSE
24	234	14.5	382 1	ICEB_XENLA
25	228.5	14.2	386 1	ICEA_XENLA
26	219.5	13.6	410 1	ICEB_FELCA
27	211.5	13.1	377 1	ICEB_BOVIN
28	210	13.0	404 1	ICEB_CANPA
29	210	13.0	418 1	ICE5_HUMAN
30	203.5	12.6	312 1	ICE2_RAT
31	199.5	12.4	404 1	ICE2_RAT
32	198	12.3	405 1	ICE2_RAT
33	197	12.2	402 1	ICE2_RAT

34	195	12.1	404 1	ICE7_HUMAN	P29466 homo sapien
35	190	11.8	373 1	ICEB_MOUSE	P70343 mus musculu
36	189	11.7	402 1	ICEB_MOUSE	P29462 mus musculu
37	184	11.4	377 1	ICE4_HUMAN	P49662 homo sapien
38	177	11.0	419 1	ICEC_MOUSE	008736 mus musculu
39	171	10.6	480 1	CEFA_HUMAN	015519 h casp8 and
40	171	10.6	484 1	CEFA_MOUSE	035732 m casp8 and
41	99.5	6.2	282 1	FA9_RAT	P16296 rattus norv
42	94.5	5.9	603 1	YB55_MENJA	058555 methanococ
43	91	5.6	1100 1	RAD1_YEAST	P06777 saccharomyc
44	89.5	5.5	459 1	FA9_MOUSE	P16294 mus musculu
45	88.5	5.5	356 1	CARA_THETN	08rbk1 thermoaer

#### ALIGNMENTS

RESULT 1	ID	ICE7_HUMAN	STANDARD:	PRT:	303 AA.
AC	P55210	013364: 096BA0			
DT	01-OCT-1996	(Rel. 34, Created)			
DT	01-OCT-1996	(Rel. 34, last sequence update)			
DT	15-JUN-2002	(Rel. 41, last annotation update)			
DE	Caspase-7 precursor (BC 3.4.22.-) (ICE-like apoptotic protease 3)				
DE	(ICE-LAP3) (Apoptotic protease Mch-3) (CMH-1).				
GN	CASP7 OR MCH3.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID-9606;				
RA	SEQUENCE FROM N.A. (ALPHA ISOFORM).				
RX	MEDLINE-96139498; PubMed-8576161;				
RA	Duan H., Chinaiyan A.M., Hudson P.L., Wing J.P., He W.-W.,				
RA	Dixit V.M.;				
RT	"ICE-LAP3, a novel mammalian homologue of the Caenorhabditis elegans				
RT	cell death protein Ced-3 is activated during Fas- and tumor necrosis				
RT	factor-induced apoptosis."				
RL	J. Biol. Chem. 271:1621-1625(1996).				
RN	[1]				
RP	SEQUENCE FROM N.A. (ALPHA ISOFORM).				
RC	TISSUE-Spleen;				
RX	MEDLINE-96147144; PubMed-8567622;				
RA	Lippe J.A., Gu Y., Sarnacki C., Caron P.R., Su M.S.-S.;				
RT	"Identification and characterization of CPP32/Mch2 homolog 1, a novel				
RT	cysteine protease similar to CPP32."				
RL	J. Biol. Chem. 271:1825-1828(1996).				
RN	[3]				
RP	SEQUENCE FROM N.A. (ALPHA AND BETA ISOFORMS).				
RC	TISSUE-T-cell;				
RX	MEDLINE-96105019; PubMed-8521391;				
RA	Fernandes-Alnemri T., Takahashi A., Armstrong R.C., Krebs J.,				
RA	Fritz L.C., Tomaselli K.J., Wang L., Yu Z., Croce C.M., Salvesson G.,				
RA	Earnshaw W.C., Litwack G., Alnemri E.S.;				
RT	"Mch3, a novel human apoptotic cysteine protease highly related to				
RT	CPP32."				
RL	Cancer Res. 55:6045-6052(1995).				
RN	[4]				
RP	SEQUENCE FROM N.A. (ALPHA AND ALPHA' ISOFORMS).				
RC	TISSUE-Petal lung, and fetal spleen;				
RX	MEDLINE-97224489; PubMed-9070923;				
RA	Juan T.S.-C., McNiece I.K., Argento J.M., Jenkins N.A., Gilbert D.J.,				
RA	Copeland N.G., Fletcher F.A.;				
RT	"Identification and mapping of Casp7, a cysteine protease resembling				
RT	CPP32 beta, interleukin-1 beta converting enzyme, and CED-3."				
RL	Genomics 40:86-93(1997).				
RN	[5]				
RP	SEQUENCE FROM N.A. (ALPHA ISOFORM).				
RC	TISSUE-Skin;				
RA	Strausberg R.;				
RL	Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.				
RN	[6]				

```

RP PROCESSING. PubMed-8755496;
RX MEDLINE-96353838;
RA Fernandes Alimenti T., Armstrong R.C., Krebs J., Srinivasula S.M., Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J., Litwak G., Alimenti E.S.;
RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human apoptotic cysteine protease containing two PAD4-like domains." Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
CC -I- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES AND ACTIVATES STEROL REGULATORY ELEMENT BINDING PROTEINS (SREBPs). PROTEOLYTICALLY CLEAVES POLY(AD-RIBOSE) POLYMERASE (PARP) AT A 216-ASP-1-GLY-217 BOND. OVEREXPRESSION PROMOTES ISRAMIN SULFONAMIDES.
CC -I- ENZYME REGULATION: INHIBITED BY ISARTIN SULFONAMIDES.
CC -I- SUBUNIT: HETERODIMER OF A 20 kDa (P20) AND A 11 kDa (P11) SUBUNIT.
CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
CC -I- ALTERNATIVE PRODUCTS: 3 ISOFORMS; ALPHA (SHOWN HERE), BETA AND ALPHA'. ARE PRODUCED BY ALTERNATIVE SPLICING. THE BETA ISOFORM IS NOT PROTEOLYTICALLY ACTIVE.
CC -I- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, SKELETAL MUSCLE, LIVER, KIDNEY, SPLEEN AND HEART, AND MODERATELY IN TESTIS. NO EXPRESSION IN THE BRAIN.
CC -I- PPM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE SUBUNTS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND VICE VERSA.
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC -I- CAUTION: WHAT WE CALL ALPHA' ISOFORM IS KNOWN IN REF.4 AS BETA, BUT AS BETA IS ALREADY DEFINED IN REF.3 WE HAVE CALLED IT ALPHA'.
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DR EMBL; U39613; AAC50346.1; -
DR EMBL; U40281; AAC50352.1; -
DR EMBL; U37448; AAC50303.1; -
DR EMBL; U37449; AAC50304.1; -
DR EMBL; U67319; AAC51152.1; -
DR EMBL; U67320; AAC51153.1; -
DR EMBL; U67206; AAF21460.1; -
DR EMBL; BC015799; AAH15799.1; -
DR HSSP; P42574; IPAU.
DR MEROPS: C14.004; -.
DR Genew; HGNC:1508; CASP7.
DR MIM: 601761; -.
DR InterPro; IPRO02398; ICE.
DR InterPro; IPRO02138; ICE_P10.
DR InterPro; IPRO01309; ICE_P20.
PFam; PF00655; ICE_P10; 1.
PFam; PF00656; ICE_P20; 1.
DR PRINTS; PR00376; TLIBCENZYM.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS_1.
DR PROSITE; PS01121; CASPASE_HIS_1.
DR PROSITE; PSS0207; CASPASE_P10; 1.
DR PROSITE; PSS0208; CASPASE_P20; 1.
KW Hydrolyase; Thiol protease; Zymogen; Apoptosis; Alternative splicing.
FT PROPEP 1 23
FT CHAIN . 24 198 CASPASE-7 SUBUNIT P20.
FT PROPEP 199 206
FT CHAIN 207 303 CASPASE-7 SUBUNIT P11.
FT ACT_SITE 144 144 BY SIMILARITY.
FT ACT_SITE 186 186
FT VARSPPLIC 1 1
FT VARSPPLIC 149 303
FT VARSPPLIC 149 303
M -> MDQVGPGRKWHLEKSCGSGSSGICASYVTQM
(VIN ISOFORM ALPHA')
VITKDGYTPFKIDTAHRNGRCCTLLAEKRLFIQAQCRGT
ELDGGIQADSDSPINDTDNPRYKIPIVENDELFATSTVPGYI

```

FT				SMBPBGSGMFWVQALCSITLSEHGKDLIMOLITRVNDRVAR
FT				HFEQSDDPHFHEKKQIPCVSMULTLEIYSO -> MESCS
FT				VTOGVGVRDGLRIQPPLPRVLAEGPSILMASRPRGSPMTQ
FT				MILDITRSOMKLSSSPIPROAITRGGADEAEGALCKPSA
FT				PMSWSTERKTMSCRSSPG (IN ISOFORM BETA).
FT	MUNAGEN	186	186	C->A: NO APOPTOTIC ACTIVITY.
FT	CONFLICT	4	4	D -> E (IN REF. 5).
FT	CONFLICT	194	194	G -> A (IN REF. 1).
SO	SEQUENCE	303 AA;	34276 MW;	_CD373EEB54A232CA4 CRC64;
	Query Match		99.6%;	Score 1606; DB 1; Length 303;
	Best Local Similarity		99.3%;	Pred. No. 1.5e-131;
	Matches 301;	Conservative 1;	Mismatches 1;	Indels 0; Gaps 0;
OY	1	MADDOGCIEEKGVEDSANEVSVDAKPRDSSEVPSLFSKRRKNVTMRISIKTTRDRVPTYQY	60	
Db	1	MADDOGCIEEKGVEDSANEVSVDAKPRDSSEVPSLFSKRRKNVTMRISIKTTRDRVPTYQY	60	
OY	61	NMNEFKLKCLIIINNKNNDKYTGACVNRGTGXDAEALFKCERSLGFDVIYNDCSCAMQ	120	
Db	61	NMNEFKLKCLIIINNKNNDKYTGACVNRGTGXDAEALFKCERSLGFDVIYNDCSCAMQ	120	
OY	121	DLTKASEEDHTNACFCFILLSGEEVVIYGKQGVPIKDLTAHFRDRCKTLLEPKL	180	
Db	121	DLTKASEEDHTNACFCFILLSGEEVVIYGKQGVPIKDLTAHFRDRCKTLLEPKL	180	
OY	181	FFIQACRGTELDIDAIOADSGPINDTDANPRXKIVPEADFLFAYSTVGYSWSRSPGRGSW	240	
Db	181	FFIQACRGTELDIDAIOADSGPINDTDANPRXKIVPEADFLFAYSTVGYSWSRSPGRGSW	240	
OY	241	FVOALCSITLSEHGKELEFMOLLTVRNDRVANHFESQSDDPHFHEKKQIPCVSMULTELY	300	
Db	241	FVOALCSITLSEHGKELEFMOLLTVRNDRVANHFESQSDDPHFHEKKQIPCVSMULTELY	300	
OY	301	FSQ 303		
Db	301	FSQ 303		
	RESULT 2			
ID	ICE7_MESAU	STANDARD;	PRT;	303 AA.
AC	P55214;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Caspase-7 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 3)			
DE	(ICE-LAP3) (Apoptotic protease Mch-3) (SREBP cleavage activity 2)			
DE	(SCA-2).			
GN	CASP7 OR MCH3.			
OS	Mesocricetus auratus (Golden hamster).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;			
OC	Mesocricetus.			
OX	NCBI_TaxID=10036;			
RN	[1]			
RN	SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.			
RP	STRAIN-Syrian; TISSUE-Liver;			
RC	MEDLINE-96224303; PubMed-8643593;			
RX	Pal J.-T., Brown M.S., Goldstein J.L.;			
RA	"Purification and cDNA cloning of a second apoptosis-related cysteine			
RT	protease that cleaves and activates sterol regulatory element binding			
RT	proteins.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 93:5437-5442(1996).			
CC	-I- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES			
CC	RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES AND ACTIVATES STEROL			
CC	REGULATORY ELEMENT BINDING PROTEINS (SERBS). PROTEOLYTICALLY			
CC	CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A 216-ASP-1-GLY-217			
CC	BOND. OVEREXPRESSION PROMOTES PROGRAMMED CELL DEATH (BY			
CC	SIMILIARITY).			
CC	-I- SUBUNIT: HETERODIMER OF A 20 kDa (#20) AND A 11 kDa (P11) SUBUNIT			
CC	(BY SIMILIARITY).			
CC	-I- SUBCELLULAR LOCATION: Cytoplasmic.			

```

CC -1- PTM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
CC SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
CC CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CC CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
CC VICE VERSA (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC -----
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CC EMBL: U47332; AAC52595.1;
CC HSSP: P42574; 1PAU.
CC MEROPS: C14.004;
CC InterPro: IPR002398; ICE.
CC InterPro: IPR002138; ICE_p10.
CC InterPro: IPR001309; ICE_p10.
CC Pfam: PF00655; ICE_p10; 1.
CC Pfam: PF00656; ICE_p20; 1.
CC PRINTS: PR00376; ILBCEZYME.
CC SMART: SM00115; CASC; 1.
CC PROSITE: PS01122; CASPASE_CYS; 1.
CC PROSITE: PS01121; CASPASE_HIS; 1.
CC PROSITE: PS50207; CASPASE_P10; 1.
CC PROSITE: PS50208; CASPASE_P20; 1.
CC Hydrolase: Thiol protease; Zymogen; Apoptosis.
CC CHAIN 1 23
CC PROPEP 24 198 CASPASE-7 SUBUNIT P20.
CC CHAIN 199 206 BY SIMILARITY.
CC CHAIN 207 303 CASPASE-7 SUBUNIT P11.
CC ACT_SITE 144 144 BY SIMILARITY.
CC ACT_SITE 186 186 BY SIMILARITY.
CC SEQUENCE 303 AA; 34037 MW; EA29356D90984648 CRC64;

Query Match 86.4%; Score 1394; DB 1; Length 303;
Best Local Similarity 84.2%; Pred. No. 3; Le-113;
Matches 255; Conservative 22; Mismatches 26; Indels 0; Gaps 0;

QY 1 MADDGCGIEGVEDSANDSVDAKPRSSFFVLSFKKKKNVYMSIKTRDRVPTQY 60
DB 1 MADDGCGIEGVEDSANDSVDAKPRSSFFVLSFKKKKNVYMSIKTRDRVPTQY 60
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QY 61 MNPEKLGKCTIIINKNKNDKVTGMVGRNCTDADAEALFCFSLGADVYYINDSCAKMQ 120
DB 61 MNPEKLGKCTIIINKNKNDKVTGMVGRNCTDADAEALFCFSLGADVYYINDSCAKMQ 120
QY 121 DLTKASEEDHTNACFACILSHSEENVYIGKDGVTPIKDLTAHFRGDRCKTLEKPKL 180
DB 121 DLTKASEEDHTNACFACILSHSEENVYIGKDGVTPIKDLTAHFRGDRCKTLEKPKL 180
QY 121 DLTKASEEDHTNACFACILSHSEENVYIGKDGVTPIKDLTAHFRGDRCKTLEKPKL 180
DB 121 DLTKASEEDHTNACFACILSHSEENVYIGKDGVTPIKDLTAHFRGDRCKTLEKPKL 180
QY 181 FFIQACRGTELDGADSGPINDTANPRYKIPVEADLFAYSTVPGYYSMRSPRGSM 240
DB 181 FFIQACRGTELDGADSGPINDTANPRYKIPVEADLFAYSTVPGYYSMRSPRGSM 240
QY 241 FVQALCSITLHENGKLEIMQITRNDKRAKRFESQSDPHHEKQICVYSMLTKELY 300
DB 241 FVQALCSITLHENGKLEIMQITRNDKRAKRFESQSDPHHEKQICVYSMLTKELY 300
QY 301 FSO 303
DB 301 FSO 303
QY 301 FGR 303
DB 301 FGR 303

RESULT 3
ID ICE7_MOUSE STANDARD: PRT: 303 AA.
AC P97864; 008669;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)

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DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Caspase-7 precursor (EC 3.4.22.-) (LICE2 cysteine protease) (Apoptotic
DE protease Mch-3).
GN CASP7 OR MCH3 OR LICE2.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Skeletal muscle;
RX MEDLINE=97224489; PubMed=9070923;
RA Juan T.-C., McNiece I.R., Argento J.M., Jenkins N.A., Gilbert D.J.,
RA Copeland N.G., Fletcher F.A.;
RT Identification and mapping of Casp7, a cysteine protease resembling
RT CPP32 beta, interleukin-1 beta converting enzyme, and CED-3";
RL Genomics 40:86-93(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97236307; PubMed=9125129;
RA Mukasa T., Khoroqui Y., Tsukahara T., Momoi M.Y., Kimura I.,
RA Momoi T.;
RT "Workmanin enhances CPP32-like activity during neuronal
RT differentiation of P19 embryonal carcinoma cells induced by retinoic
RT acid.";
RL Biochem. Biophys. Res. Commun. 232:192-197(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/An;
RX MEDLINE=97190206; PubMed=9038361;
RA van de Graen M., Vandenaebale P., Declercq W., van den Brande I.,
RA van Looy G., Molemans F., Schotte P., van Criekinge W., Beyaert R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members.";
RL FEBS Lett. 403:61-69(1997).
RN [4]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
CC RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES AND ACTIVATES STEROL
CC REGULATORY ELEMENT BINDING PROTEINS (SREBPS). OVEREXPRESSION
CC PROMOTES PROGRAMMED CELL DEATH (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF A 20 kDa (P20) AND A 11 kDa (P11) SUBUNIT.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, LUNG, LIVER, AND
CC KIDNEY. LOW LEVELS IN SPLEEN, SKELETAL MUSCLE, AND TESTIS. NO
CC EXPRESSION IN THE BRAIN.
CC -1- PTM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
CC SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
CC CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CC CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
CC VICE VERSA (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
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CC -----
CC EMBL: U67321; AAC33068.1; ALT_INIT.
CC EMBL: D86353; BAAL9730.1;
CC EMBL: Y13088; CAAT3530.1;
CC EMBL: BC005428; AAH05428.1;
CC HSSP: P42574; 1PAU.
CC MEROPS: C14.004;
CC MGD: MGT:109383; Casp7.
CC InterPro: IPR002398; ICE.
CC InterPro: IPR002138; ICE_p10.
CC InterPro: IPR001309; ICE_p20.

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DR	Pfam: PF00655; ICE_p10: 1.	
DR	Pfam: PF00656; ICE_p20: 1.	
DR	PRINTS: PR00376; IILIBENZYME.	
DR	SMART: SM00115; CASG: 1.	
DR	PROSITE: PS01122; CASPASE_CYS: 1.	
DR	PROSITE: PS01121; CASPASE_HIS: 1.	
DR	PROSITE: PS50207; CASPASE_P10: 1.	
DR	PROSITE: PS50208; CASPASE_P20: 1.	
KM	Hydrolase: Thiol protease; Zymogen: Apoptosis.	
FT	PROPEP	1 23
FT	CHAIN	24 198
FT	PROPEP	199 206
FT	CHAIN	207 303
FT	ACT_SITE	144 144
FT	ACT_SITE	186 186
FT	CONFLICT	10 11
FT	CONFLICT	45 45
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SQ	SEQUENCE	303 AA: 34060 MW: 747787b5bde5f744 CRC64:

RESULT 5  
ICE3\_HUMAN STANDARD; PRT; 277 AA.  
AC P42574;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Apoptin precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama  
protein) (CPP-32) (Caspase-3) (SREBP cleavage activity 1)  
DE (SCA-1).  
GN CASP3 OR CPP32.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RP SEQUENCE FROM N.A. (ALPHA AND BETA ISOFORMS).  
RC TISSUE=T-cell;  
RX MEDLINE=95074098; PubMed=7983002;  
RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;  
RT "CPP32, a novel human apoptotic protein with homology to  
Caenorhabditis elegans cell death protein Ced-3 and mammalian  
interleukin-1 beta-converting enzyme.";  
RL J. Biol. Chem. 269:30761-30764(1994).  
[2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95292347; PubMed=7774019;  
RA Tewari M., Quan L.T., O'Rourke K., Desnoyers S., Zeng Z.,  
RT Belder D.R., Porter G.G., Salvesen G.S., Dixit V.M.;  
RT "Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable  
protease that cleaves the death substrate poly(ADP-ribose)  
polymerase.";  
RL Cell 81:801-809(1995).  
[3]  
RP SEQUENCE OF 29-46 AND 175-193, AND FUNCTION.  
RX MEDLINE=95319529; PubMed=7596430;  
RA Nicholson D.W., Ali A., Thornberry N.A., Vailancourt J.P., Ding C.K.,  
RT Gallant M., Gareau Y., Griffin P.R., Labelle M., Lazebnik Y.A.,  
RA Munday N.A., Raju S.M., Smulson M.E., Yamin T.-T., Li V.L.,  
RA Miller D.K.;  
RT "Identification and inhibition of the ICE/CED-3 protease necessary  
for mammalian apoptosis.";  
RL Nature 376:37-43(1995).  
[4]  
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 28-277.  
RX MEDLINE=96263532; PubMed=8673606;  
RA Rotonda J., Nicholson D.W., Fazil K.M., Gallant M., Gareau Y.,  
RT Labelle M., Peterson E.P., Rasper D.M., Ruel R., Vailancourt J.P.,  
RA Thornberry N.A., Becker J.W.;  
RT "The three-dimensional structure of apoptin/CPP32, a key mediator of  
apoptosis.";  
RL Nat. Struct. Biol. 3:619-625(1996).  
[5]  
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 35-173 AND 185-277.  
RX MEDLINE=97197830; PubMed=9045680;  
RA Mittl P.R., di Marco S., Krebs J.F., Bai X., Karanewsky D.S.,  
RT Priestle J.P., Tomaselli K.J., Grutter M.G.;  
RT Structure of recombinant human CPP32 in complex with the  
tetrapeptide acetyl-Asp-Val-Ala-Asp fluoromethyl ketone.";  
RL J. Biol. Chem. 272:6539-6547(1997).  
[6]  
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).  
RX MEDLINE=20283632; PubMed=10821855;  
RA Lee D., Long S.A., Adams J.L., Chan G., Valda K.S., Francis T.A.,  
RT Kikly K., Winkler J.D., Sung C.-M., Debouck C., Richardson S.,  
RA Levy M.A., Demolf W.E. Jr., Keller P.M., Tomaszek T., Head M.S.,  
RT Ryan M.D., Haltiwanger R.C., Liang P.H., Janson C.A., McDevitt P.J.,  
RA Johanson K., Concha N.O., Chan W., Abdel-Meguid S.S., Badger A.M.,  
RT Lark M.W., Nadeau D.P., Suva L.J., Gowen M., Nuttall M.E.;  
RT "Potent and selective nonpeptide inhibitors of caspases 3 and 7  
inhibit apoptosis and maintain cell functionality.";

RL J. Biol. Chem. 275:16007-16014(2000).  
[7]  
RN PROCESSING.  
RP MEDLINE=96353838; PubMed=8755496;  
RX Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,  
RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,  
RA Litwack G., Alnemri E.S.;  
RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human  
apoptotic cysteine protease containing two FADD-like domains.";  
RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).  
[8]  
RP CLEAVAGE OF HUNTINGTIN.  
RX MEDLINE=9631285; PubMed=8696339;  
RA Goldberg Y.P., Nicholson D.W., Rasper D.M., Kalchman M.A., Koide H.B.,  
RA Graham R.K., Bromm M., Kazemi-Esfarjani P., Thornberry N.A.,  
RA Vailancourt J.P., Hayden M.R.;  
RT "Cleavage of huntingtin by apoptin, a proapoptotic cysteine protease,  
is modulated by the polyglutamine tract.";  
RL Nat. Genet. 13:442-449(1996).  
[9]  
CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES  
RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT  
PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A  
216-ASP-1-GLY-217 BOND. CLEAVES AND ACTIVATES STEROL REGULATOR  
ELEMENT BINDING PROTEINS (SREBPs) BETWEEN THE BASIC HELIX-LOOP-  
HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.  
CC CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9. INVOLVED IN THE  
CLEAVAGE OF HUNTINGTIN.  
CC -1- ENZYME REGULATION: INHIBITED BY ISATIN SULFONAMIDES.  
CC -1- SUBUNIT: HETERODIMER OF A 17 kDa (P17) AND A 12 kDa (P12) SUBUNIT.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, SPLEEN, HEART, LIVER  
AND KIDNEY. MODERATE LEVELS IN BRAIN AND SKELETAL MUSCLE. AND LOW  
IN TESTES. ALSO FOUND IN MANY CELL LINES. HIGHEST EXPRESSION IN  
CELLS OF THE IMMUNE SYSTEM.  
CC -1- PTM: CLEAVAGE BY GRANZYME B, APAF-1, CASPASE-6, -8 AND -10  
GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE  
PROPEPTIDES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE  
ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT  
OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR  
AND VICE VERSA.  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.  
CC -----  
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DR EMBL: U13737; AAA65015.1; -;  
DR EMBL: U13738; AAB60355.1; -;  
DR EMBL: U26943; AA74929.1; -;  
DR PDB: 1PAU; 07-JUL-97.  
DR PDB: 1CP3; 24-DEC-97.  
DR PDB: 1GFM; 23-JUN-00.  
DR MEROPS: C14.003; -;  
DR Genew: HGNC:1504; CASP3.  
DR MIM: 600636; -;  
DR InterPro: IPR002398; ICE.  
DR InterPro: IPR002138; ICE\_P10.  
DR InterPro: IPR001309; ICE\_P20.  
DR Pfam: PF00655; ICE\_P10; 1.  
DR Pfam: PF00656; ICE\_P20; 1.  
DR PRINTS: PRO0376; ILIHCENYME.  
DR SMART: SM00115; CASC.1.  
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DR PROSITE: PS01121; CASPASE\_HIS; 1.  
DR PROSITE: PS50207; CASPASE\_P10; 1.  
DR PROSITE: PS50208; CASPASE\_P20; 1.  
KW Hydrolase; Thiol protease; Zymogen; Apoptosis; Polymorphism;  
KW 3D-structure. 1 9  
FT PROPEP





FT CONFLICT 236 236 L -> I (IN REF. 4).  
FT CONFLICT 245 245 T -> M (IN REF. 3).  
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Query Match  
Best Local Similarity 50.3%; Pred. No. 1.1e-54;  
Matches 144; Conservative 44; Mismatches 82; Indels 16; Gaps 3;  
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Db 230 LEFMHILTRVNRKRVATEPFESFLDAPFAKKQIPCIYSMLTKELXF 275  
RESULT 7  
ID ICE3\_MOUSE STANDARD: PRT: 277 AA.  
AC P70677: 008668:  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Apolipin precursor (EC 3.4.22.-) (Cysteine protease Cpp32) (Yama  
DE protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)  
DE (SCA-1) (ICE).  
DE CASP3 OR CPP32.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96358624; PubMed=8761296;  
RA Juan T.S.C., McNelece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G.,  
RA Fletcher F.A.;  
RT "Molecular characterization of mouse and rat CPP32 beta gene encoding  
RT a cysteine protease resembling interleukin-1 beta converting enzyme  
RT and CED-3.";  
RL Oncogene 13:749-755(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97224429; PubMed=9070890;  
RA Mukasa T., Urase K., Momoi M.Y., Kimura I., Momoi T.;  
RT "Specific expression of Cpp32 in sensory neurons of mouse embryos and  
RT activation of Cpp32 in the apoptosis induced by a withdrawal of  
RT NGF.";  
RL Biochem. Biophys. Res. Commun. 231:770-774(1997).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX STRAIN=C3H/An;  
RA MEDLINE=97190206; PubMed=9038361;  
RX van de Craen M., Vandenaabee P., Declercq W., van den Brande I.,  
RA van Looy G., Molemans F., Schotte P., van Crielinge W., Bejaert R.,  
RA Fiers W.;  
RT "Characterization of seven murine caspase family members.";  
RL FEBS Lett. 403:61-69(1997).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;

RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;  
RL Submitted (May 1997) to the EMBL/GenBank/DBD databases.  
CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES  
CC RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT  
CC PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A  
CC 216-ASP-1-GLY-217 BOND. CLEAVES AND ACTIVATES STEROL REGULATOR  
CC ELEMENT BINDING PROTEINS (SREBPs) BETWEEN THE BASIC HELIX-LOOP-  
CC HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.  
CC CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9 (BY SIMILARITY).  
CC CLEAVES IL-1 BETA BETWEEN AN ASP AND AN ALA, RELEASING THE MATURE  
CC CYTOKINE WHICH IS INVOLVED IN A VARIETY OF INFLAMMATORY PROCESSES.  
CC -1- SUBUNIT: HETERODIMER OF A 17 KDA (P17) AND A 12 KDA (P12) SUBUNIT  
CC (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: HIGHEST EXPRESSION IN SPLEEN, LUNG, LIVER,  
CC KIDNEY AND HEART. LOWER EXPRESSION IN BRAIN, SKELETAL MUSCLE AND  
CC TESTIS.  
CC -1- PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE  
CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS  
CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED  
CC PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF  
CC CASPASE-7 (PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND  
CC VICE VERSA (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.  
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CC  
CC EMBL: U54803; AAC52768.1; -;  
CC EMBL: U54802; AAC52768.1; JOINED.  
CC EMBL: U49929; AAC52764.1; -;  
CC EMBL: D86352; BAA21727.1; -;  
CC EMBL: Y13086; CA73528.1; -;  
CC EMBL: U19522; AAC53196.1; -;  
CC HSSP: P42574; 1PAU.  
CC DR MEROPS: C14.003; -;  
CC MGD: MG1:107739; Casp3.  
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CC DR InterPro: IPR002138; ICE\_P10.  
CC DR InterPro: IPR001309; ICE\_P20.  
CC DR Pfam: PF00655; ICE\_P10; 1.  
CC DR Pfam: PF00656; ICE\_P20; 1.  
CC DR PRINTS: PR00376; ILIBENZYM.  
CC SMART: SM00115; CASC.1.  
CC PROSITE: PS01122; CASPASE\_CTS; 1.  
CC PROSITE: PS01121; CASPASE\_HIS; 1.  
CC DR PROSITE: PS50207; CASPASE\_P10; 1.  
CC DR PROSITE: PS50208; CASPASE\_P20; 1.  
CC KW Hydrolyase; Thiol protease; zymogen; Apoptosis.  
CC FT PROPEP 1 9  
CC FT PROPEP 10 28  
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CC FT ACT\_SITE 121 121  
CC FT ACT\_SITE 163 163  
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CC FT CONFLICT 84 84  
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CC FT CONFLICT 97 97  
CC FT CONFLICT 128 128  
CC FT CONFLICT 135 135  
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Best Local Similarity 43.6%; Score 703; DB 1; Length 277;  
Matches 146; Conservative 40; Mismatches 83; Indels 18; Gaps 4;



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EMBL: U81510; AAC47442.1; -

HSSP: P42574; ICP3.

DR MEROPS: C14.015; -

DR InterPro: IPR002398; ICE.

DR InterPro: IPR002138; ICE\_P10.

DR InterPro: IPR001309; ICE\_P20.

DR Pfam: PF00655; ICE\_P10; 1.

DR Pfam: PF00656; ICE\_P20; 1.

DR SMART: SM00115; CASC; 1.

DR PROSITE: PS01122; CASPASE\_CYS; 1.

DR PROSITE: PS01121; CASPASE\_HIS; 1.

DR PROSITE: PS00207; CASPASE\_P10; 1.

DR PROSITE: PS00208; CASPASE\_P20; 1.

DR Hydrolyase: Thiol protease; Zymogen; Apoptosis.

FT PROPP 1 28

FT CHAIN 29 184 CASPASE-1 SUBUNIT P19/18.

FT PROPP 185 195 POTENTIAL.

FT CHAIN 196 299 CASPASE-1 SUBUNIT P12.

FT ACT\_SITE 136 136 BY SIMILARITY.

FT ACT\_SITE 178 178 BY SIMILARITY.

FT SITE 178 178 BY SIMILARITY.

SEQUENCE 299 AA: 33527 MW: 99FAFED09B04EED6 CRC64:

Query Match 34.2%; Score 552; DB 1; Length 299;

Best Local Similarity 40.5%; Pred. No. 1,8e-40;

Matches 122; Conservative 52; Mismatches 109; Indels 18; Gaps 7;

12 GVSDSANEDSVDAKP-----DRSSFVPSLFSSKKKKVTVRSIKTTDRPTPTQYNNFE 65

4 GKQDNGNVDSDIKQRTNGGDEGDLGSSSSOPNRYAMPV---DRNAPY-TNNMHK 58

66 KLGKCIITNNKNDKYTGMGVNGRTGDADALFKCFERSLGFDVIVYNDSCAKMODLLKK 125

59 HRGMALIFNHEHD-ILSLKSRFTGTVNDNLKLVKLTGFKVTFEFLNLSSEELNKFIQ 117

126 ASEDHTNACFCILLSSHEENVITGKGVTPKIDLTANFRGDRCKTLLEKPLFIQA 185

118 TAMDHSDDCLLVAVLTGELMLYAKDPHYKPDNLMYFTADKCPPLGKPLFIQA 177

186 CRCTEDDAIADSGPINDDAMP--RYKIPVEADFLFAYSTVPGYYSWSPGSGMFVQ 243

178 CQDRLDGGITLSTR---TEIDSGPSSTYRIPLVHADFLIATSTVPGYYSWNTTSGSMFQ 234

244 ALCSILEHGKLEIMQILRVNDRVRAHRESOS-DDPHFEKKOIPCVYSMLTKELYES 302

235 ALCEELRYAGTERDITLLTLFVQGVKVALDESNAPDSAMHQQKQVPCITSMLTRLLVFG 294

303 Q 303

295 K 295

RESULT 10

ICE\_DROME STANDARD; PRT; 339 AA.

01-NOV-1997 (Rel. 35, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

Caspase precursor (EC 3.4.22.-) (drICE).

ICE OR CG7788.

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI\_TaxID=7271;

SEQUENCE FROM N.A.

TISSUE=Embryo;

MEDLINE=97327558; PubMed=9184225;

Fraser A.G., Evan G.I.;

"Identification of a Drosophila melanogaster ICE/CED-3-related

protease, drICE.";

EMBO J. 16:2805-2813(1997).

[2]

SEQUENCE FROM N.A.

STRAIN=Berkeley;

MEDLINE=20196006; PubMed=10731137;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Amanalides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Mortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,

Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.C.,

Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

Bailey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

Borkova D., Botchan M.R., Bouch J., Broksstein P., Brotler P.,

Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

de Paulis B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

Durbin K.J., Evangelista C.C., Ferraz C., Ferriere S., Fleischmann W.,

Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

GAJDEK A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Hoslin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,

Mout S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclob J.M.,

Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

Rabinet K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

Spieler E., Spradling A.C., Stapleton M., Strong R., Sun E.,

Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,

Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA GIBBS R.A., Myers E.W., Rubin G.M., Venter J.C.;

"The genome sequence of Drosophila melanogaster.";

Science 287:2185-2195(2000).

-1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES

RESPONSIBLE FOR APOPTOSIS EXECUTION. ACTS DOWNSTREAM OF RPR.

CC CLEAVES BACULOVIRUS P35 AND LAMIN DMO IN VITRO.

-1- SUBUNIT: HETERODIMER OF A 21 kDa (P21) AND A 12 kDa (P12) SUBUNIT.

-1- DEVELOPMENTAL STAGE: EXPRESSED AT ALL STAGES WHERE APOPTOSIS

OCCURS.

-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.

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EMBL: Y12261; CAAT2937.1; -

EMBL: AE003771; AAF56939.1; -

HSSP: P42574; IPAU.

DR HSSP: P42574; ICP3.

DR MEROPS: C14.015; -

DR Pfam: PF00655; ICE\_P10; 1.

DR InterPro: IPR002398; ICE.

DR InterPro: IPR002138; ICE\_P10.

DR InterPro: IPR001309; ICE\_P20.

DR Pfam: PF00655; ICE\_P10; 1.

DR Pfam: PF00656; ICE\_P20; 1.

DR PRINTS: PR00376; ILICEZYME.

DR SMART: SM00115; CASC; 1.

DR PROSITE: PS01122; CASPASE\_CYS; 1.



```

FT CHAIN 34 202 CASPASE-1 SUBUNIT P22.
FT PROPEP 203 215
FT CHAIN 216 323 CASPASE-1 SUBUNIT P13.
FT ACT_SITE 154 154 BY SIMILARITY.
FT ACT_SITE 196 196 BY SIMILARITY.
SQ SEQUENCE 323 AA; 35926 MW; B5F0FF75EB8E2BD CRC64;

Query Match 33.08; Score 532.5; DB 1; Length 323;
Best Local Similarity 44.68; Pred. No. 9, 5e-39;
Matches 111; Conservative 47; Mismatches 80; Indels 11; Gaps 6;

OY 59 OYNNNEKIKGKCIINNNKNDKVTGMGVRNGTDKDAALCKCRSLGFDYIVYNDSCAK 118
DB 70 ETNMSKHNGVALIFNHEFPD-IPSLKSRGTGVNDQELKAFENLGFVSVHDC---K 125
OY 119 MODLLK---KASEEDHTNACFACILLSHGEENVYKGDVTPDKDTLTAHFRDRCKTL 175
DB 126 LBDLKHVGKAAELDHTDNDCLAVALLSHGHEHYLAKDQYKLDNIWIKFTATFCPSLA 185
OY 176 EKPKLFFIACRGTELDDAIQADSGPINDTD--ANPRYKIPVADFLFAYSTVPGYYSWR 233
DB 186 GKPKLFFIACRGDRIDGITLEKG-VTETDGESESTSYKIPHADFLFSYSTIPGVESWR 244
OY 234 SGRGSMFVQALCSILEHCKELEIMQILTRVNDVRAHRESO-SDDPHFEKKQIPCV 292
DB 245 NINNGSMWYOSLIRELNANGKKYDLTLTLTFVNOVALDFESNVPAIPMDRQKQIPCLT 304
OY 293 SMLTKELYF 301
DB 305 SMLTKELRF 313

RESULT 12
ICE6_MOUSE STANDARD: PRT: 276 AA.
AC 008738:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Caspase-6 precursor (EC 3.4.22.-) (Apoptotic protease Mch-2).
GN CASP6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/An;
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandenaebelle P., Declercq W., van den Brande I.,
RA van Looy G., Molemans F., Schotte P., van Crielinge W., Beyaert R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members.";
RL FEBS Lett. 403:61-69(1997).
CC -I- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
CC RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES POLY(ADP-RIBOSE)
CC POLYMERASE IN VITRO, AS WELL AS LAMINS. OVEREXPRESSION PROMOTES
CC PROGRAMMED CELL DEATH (BY SIMILARITY).
CC -I- SUBUNIT: HETERODIMER OF A 18 kDa (P18) AND A 11 kDa (P11) SUBUNIT
CC (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
CC -I- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, LIVER, KIDNEY,
CC TESTIS, AND HEART. LOWER LEVELS IN SPLEEN, SKELETAL MUSCLE, AND
CC BRAIN.
CC -I- PM: CLEAVAGES BY CPP32, CASPASE-8 OR -10 GENERATE THE TWO ACTIVE
CC SUBUNITS (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Y13087; CAA73529.1; -.
DR HSSP: P42574; 1PAU.
DR MEROPS; C14.005; -.
DR MGD; MGI:131292L; Casp6.
DR Interpro: IPR002398; ICE.
DR Interpro: IPR002138; ICE_P10.
DR Interpro: IPR001309; ICE_P20.
DR Pfam; PF00655; ICE_P10; 1.
DR Pfam; PF00656; ICE_P20; 1.
DR PRINTS; PR00376; IL1BCENZME.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR Hydrolase; Thiol protease; Apoptosis; Zymogen.
FT CHAIN 1 6 162
FT PROPEP 163 176
FT CHAIN 177 276
FT ACT_SITE 104 104 BY SIMILARITY.
FT ACT_SITE 146 146 BY SIMILARITY.
SQ SEQUENCE 276 AA; 31595 MW; 5965DE9321126B6C CRC64;

Query Match 30.08; Score 483.5; DB 1; Length 276;
Best Local Similarity 38.84; Pred. No. 1, 3e-34;
Matches 99; Conservative 43; Mismatches 104; Indels 9; Gaps 2;

OY 56 PTYOYNNNEFKKCIINNNKNDKVTGMGVRNGTDKDAALFCFSLGFDYIVYNDSCS 115
DB 16 PAEOYKMDKRRGVALIFNHEFPD-IPSLKSRGTGVNDQELKAFENLGFVSVHDC---K 125
OY 116 CAMMODLLKRASEEDHTNACFACILLSHGEENVYKGDVTPDKDTLTAHFRDRCKTL 175
DB 76 AEELLLKIHVSTSSSHIDACFCIFLSHGNGNVAVADKIELQTLGLFGKGCOSLV 135
OY 176 EKPKLFFIACRGTELDDAI-----QADS-GPINDTDANPRYKIPVADFLFAYSTV 226
DB 136 GKPKLFFIACRGSDHDPVPPVPLDMVDHQTDLNDVTQVDAASYTLFAGADFLMCYSVA 195
OY 227 PGYYSRSPRGSMFVQALCSILEHCKELEIMQILTRVNDVRAHRESODDPHFHEKK 286
DB 196 EGYTSHRETVNGSMYIQDLCMLARYGSLFETELLTVNKKYSORRVDFCKDPAIGKK 255
OY 287 QIPCVVSMLELYF 301
DB 256 QVPCFASMLTKLHF 270

RESULT 13
ICE6_HUMAN STANDARD: PRT: 293 AA.
AC P55212:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Caspase-6 precursor (EC 3.4.22.-) (Apoptotic protease Mch-2).
GN CASP6 OR MCH2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE=95316841; PubMed=7796396;
RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
RT "Mch2, a new member of the apoptotic Ced-3/Ice cysteine protease gene
RT family.";
RL Cancer Res. 55:2737-2742(1995).

```







DB 292 IVEILKIVOLMDHNMDCPTICCLISGDKGIITGTDGQAPDIYELTSQFTGLKCPSLACK 351  
 QY 178 PRLFTIACRGTELDIAQADSGPINDTDAMP-----RYKIPYEADELFAVSTV 226  
 DB 352 PVEFTIACQAGNYQKGIIVET-----DSEQPYLEMDLSSPPRY-IPDEADFLMGATV 406  
 QY 227 PCTYSMRSGRGSRVFOALCSILEEH-GAELEMLQILTRYNDVRANHFESQSDPPHHEK 285  
 DB 407 NNCVSYRNMECTWYIQSICSLRERCPRGDDITLITLTVN-----YEVSNRDKKNNMG 460  
 QY 286 KQPCVSMLEKLEYF 301  
 DB 461 KQMPQPTFLRKLVF 476

RESULT 15  
 ICEA\_HUMAN  
 ID ICEA\_HUMAN STANDARD: PR1: 521 AA.  
 AC 092851: 092845: 091206: 091207:  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Caspase-10 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 4)  
 DE (Apoptotic protease Mch4) (Fas-associated DEATH domain protein  
 DE Interleukin-1B-converting enzyme 2) (FLICE2).  
 GN CASP10 OR MCH4.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM A).  
 RC TISSUE=T-cell;  
 RX MEDLINE=9635383; PubMed=8755496;  
 RA Fernandes-Alnemri T., Armstrong R.C., Krebs J., Stiniwasla S.M.,  
 RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,  
 RA Litwack G., Alnemri E.S.;  
 RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human  
 RT apoptotic cysteine protease containing two FADD-like domains";  
 RT Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).  
 RL [2]  
 RP SEQUENCE FROM N.A. (ISOFORM B).  
 RC TISSUE=Thymus, and Spleen;  
 RX MEDLINE=97197836; PubMed=9045686;  
 RA Vincenz C., Dixit V.M.;  
 RT "Fas-associated death domain protein interleukin-1beta-converting  
 RT enzyme 2 (FLICE2), an ICE/Ced-3 homologue, is proximally involved in  
 RT CD95- and p55-mediated death signaling";  
 RT J. Biol. Chem. 272:6578-6583(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORMS B AND C).  
 RC TISSUE=Thymus, and Spleen;  
 RX MEDLINE=99214592; PubMed=10187817;  
 RA Ng P.W., Porter A.G., Janicke R.O.;  
 RT "Molecular cloning and characterization of two novel pro-apoptotic  
 RT isoforms of caspase-10";  
 RT J. Biol. Chem. 274:10301-10308(1999).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM A).  
 RC MEDLINE=21100893; PubMed=11161814;  
 RA Hadano S., Yanagisawa Y., Skaug J., Fichter K., Nasir J.,  
 RA Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,  
 RA Ikeda J.-E., Hayden M.R.;  
 RT "Cloning and characterization of three novel genes, ALS2CRL, ALS2CRL2,  
 RT and ALS2CR3, in the juvenile amyotrophic lateral sclerosis (ALS2)  
 RT critical region at chromosome 2q33-q34: candidate genes for ALS2";  
 RT Genomics 71:200-213(2001).  
 RL [5]  
 RP PARTIAL SEQUENCE, AND PROCESSING.  
 RX MEDLINE=97121412; PubMed=8962078;  
 RA Stiniwasla S.M., Ahmad M., Fernandes-Alnemri T., Litwack G.,  
 RA Alnemri E.S.;  
 RT "Molecular ordering of the Fas-apoptotic pathway: the Fas/APO-1  
 RT protease Mch5 is a Crma-inhibitable protease that activates multiple

RT Ced-3/ICE-like cysteine proteases";  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:14486-14491(1996).  
 CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES  
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. RECRUITED TO BOTH FAS- AND  
 CC TNFR-1 RECEPTORS IN A FADD DEPENDENT MANNER. MAY PARTICIPATE IN  
 CC THE GRANZYME B APOPTOTIC PATHWAYS. CLEAVES AND ACTIVATES CASPASE-  
 CC 3, -4, -6, -7, -8, AND -9. HYDROLYZES THE SMALL- MOLECULE  
 CC SUBSTRATES, TYR-VAL-ALA-ASP-1-AMC AND ASP-GLU-VAL-ASP-1-AMC.  
 CC -1- FUNCTION: ISOFORM C IS PROTEOLYTICALLY INACTIVE.  
 CC -1- SUBUNIT: HETERODIMER OF A 23/17 kDa (P23/17) DEPENDENT ON THE  
 CC SPLICING EVENTS AND A 12 kDa (P12) SUBUNIT.  
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: A/10-A (SHOWN HERE), B/10-B AND  
 CC C/10-C; ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC TISSUE SPECIFICITY: DETECTABLE IN MOST TISSUES. LOWEST EXPRESSION  
 CC IS SEEN IN BRAIN, KIDNEY, PROSTATE, TESTIS, AND COLON.  
 CC -1- PTM: CLEAVAGE BY GRANZYME B AND AUTOCATALYTIC ACTIVITY GENERATE  
 CC THE TWO ACTIVE SUBUNITS.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.  
 CC -1- SIMILARITY: CONTAINS 2 DEATH EFFECTOR DOMAINS (DED).  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: U60519; AAC50644.1; -  
 DR EMBL: U66214; AAB46730.1; -  
 DR EMBL: AF111344; AAD28402.1; -  
 DR EMBL: AF111345; AAD28403.1; -  
 DR EMBL: AB038979; BAB32554.1; -  
 DR EMBL: AB038973; BAB32554.1; JOINED.  
 DR EMBL: AB038974; BAB32554.1; JOINED.  
 DR EMBL: AB038975; BAB32554.1; JOINED.  
 DR EMBL: AB038976; BAB32554.1; JOINED.  
 DR EMBL: AB038977; BAB32554.1; JOINED.  
 DR HSP: Q15806; I0DU.  
 DR MEROPS: C14.011; -  
 DR GeneW: HGNC:1500; CASP10.  
 DR MIM: 601762; -  
 DR InterPro: IPR001875; DED.  
 DR InterPro: IPR002398; ICE.  
 DR InterPro: IPR002388; ICE\_P10.  
 DR InterPro: IPR001309; ICE\_P20.  
 DR Pfam: PF00655; ICE\_P10; 1.  
 DR Pfam: PF00656; ICE\_P20; 1.  
 DR Pfam: PF01335; DED; 2.  
 DR PRINTS: PR00376; ILICENZYMHE.  
 DR SMART: SM00115; CASc; 1.  
 DR SMART: SM00031; DED; 2.  
 DR PROSITE: PS01122; CASPASE\_CYS; 1.  
 DR PROSITE: PS01121; CASPASE\_HIS; 1.  
 DR PROSITE: PS50207; CASPASE\_P10; 1.  
 DR PROSITE: PS50208; CASPASE\_P20; 1.  
 DR PROSITE: PS50168; DED; 2.  
 KW Hydrolyase; Thiol protease; Apoptosis; Zymogen; Repeat;  
 KW Alternative splicing.  
 FT CHAIN 1 219  
 FT PROPEP 1 415  
 FT CHAIN 220 415  
 FT CHAIN 416 521  
 FT CHAIN 19 97  
 FT DOMAIN 114 187  
 FT DOMAIN 358 358  
 FT ACT\_SITE 401 401  
 FT ACT\_SITE 429 271  
 FT VARSPIC 473 521  
 FT VARSPIC 241 273  
 FT VARSPIC 241 273  
 FT CASPASE-10 SUBUNIT P23/17.  
 FT CASPASE-10 SUBUNIT P12.  
 FT DED 1.  
 FT DED 2.  
 FT BY SIMILARITY.  
 FT BY SIMILARITY.  
 FT MISSING (IN SHORT ISOFORM).  
 FT MUKLEKTEINERKRTVGAQISATISPLAISQTPRP  
 FT MRRMSSV -> HEDILSLITGVNDVSRDQCKTKQMP  
 FT OPATFLRKLVFPVPLDALSI (IN ISOFORM B).  
 FT GNRATNGAPSLVSRMGASANTLNSSTSKRA -> EGSC  
 FT VODESEPRPLCHCQOPOLYLPEQGTNRNP (IN ISOFORM  
 FT C).

FT VARSPIC 274 521 MISSING (IN ISOPFORM C).  
FT CONFLICT 68 68 E -> G (IN REF. 2).  
FT CONFLICT 268 268 T -> A (IN REF. 3).  
FT CONFLICT 410 410 V -> I (IN REF. 3).  
SQ SEQUENCE 521 AA; 58950 MW; 840348AE602B243 CRC64;

Query Match 24.5%; Score 395; DB 1; Length 521;  
Best Local Similarity 30.4%; Pred. No. 1.3e-26;

Matches 95; Conservative 55; Mismatches 99; Indels 64; Gaps 9;

QY 11 QGVEDSANEDSV---DAKPDRS-----SFVPSLFSKKKKNTMRSI--KT 50  
Db 209 QGEELVYSQTDVKTFLPALPOESMOKNHAGSNGNRATNGAPSLVSRGMOGASANTLNSET 268  
QY 51 TDREVPPTYQYNMNEFKLGKCIINNKNFDKVTGMGVNGTDDKDAEALFKCFRSLGFDVIV 110  
Db 269 STKRAAVYRRNRRNR--GLCVIVNHSF---TSLKDRGTHKDAELLSHVQWLGFTVHI 323  
QY 111 YNDCSCAKMODLKKAS-EEDHTNACFPACILLSHGEEENVYGRD-GVTPIKDLTAHFRG 168  
Db 324 HNNVTKMEMEMVLQKCKNPNHADGDFVFCILTHGRFGAVYSSDEALIPIREIMSHPTA 383  
QY 169 DRCKTLLEKPKLFIFQCRGTETLDDAIQADSGPINDTA--NPRYKIPVEADFLFAISTV 226  
Db 384 LQCPRLAEKPKLFIFQACQGEELIOPSVSIEADALNPEQAPTSLQDSIPAEDFLGLATV 443  
QY 227 PGYYSNRSFGRGSMFVOALCSILEHGEKELEIMQILTRVNDRAVHRHESQSDDPHFHEKK 286  
Db 444 PGYVSFRHVEGSMYIOSLCN-----HLKK 468  
QY 287 QIPCVVSMLTREL 299  
Db 469 LVPRLMLKFLKTM 481

Search completed: December 2, 2002, 12:56:29  
Job time : 11.4483 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 2, 2002, 12:54:49 ; Search time 28.7328 Seconds  
(without alignments)  
2172.860 Million cell updates/sec

Title: US-09-895-263-2

Perfect score: 1613  
Sequence: 1 MADQGCIEEGVDSANED.....EKKQPCVSMILKELYFSQ 303

Scoring table: BL0SUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: SP:REMBL\_21:\*  
2: SP:archaea:\*  
3: SP:bacteria:\*  
4: SP:fungi:\*  
5: SP:human:\*  
6: SP:invertebrate:\*  
7: SP:mammal:\*  
8: SP:mhc:\*  
9: SP:organelle:\*  
10: SP:phage:\*  
11: SP:plant:\*  
12: SP:rodent:\*  
13: SP:vertebrate:\*  
14: SP:unclassified:\*  
15: SP:virus:\*  
16: SP:bacteriophage:\*  
17: SP:archaeo:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1395	86.5	303	11 088550	088550 ratius norv
2	1025	63.5	318	13 091B65	091B65 xenopus lae
3	744.5	46.2	282	13 098U18	098U18 brachydanio
4	743	46.1	283	13 093417	093417 gallus gall
5	721	44.7	277	4 096AN1	096AN1 homo sapien
6	720.5	44.7	277	6 095ND5	095ND5 sus scrofa
7	719	44.6	277	4 096KP2	096KP2 homo sapien
8	623.5	38.7	220	11 090W14	090W14 mus musculu
9	512.5	31.8	304	13 091B66	091B66 xenopus lae
10	510	31.0	302	13 091B59	091B59 xenopus lae
11	500.5	30.6	182	6 077623	077623 ovis aries
12	493.5	30.0	276	11 099M47	099M47 mus musculu
13	483.5	29.8	277	11 035397	035397 ratius norv
14	481	29.4	293	4 0980E7	0980E7 homo sapien
15	474	29.4	276	11 090D89	090D89 mus musculu
16	473.5	29.4	276	11 090D89	090D89 mus musculu

17	447.5	27.7	480	11 089110	089110 m caspase 8
18	446.5	27.7	482	13 090W01	090W01 gallus gall
19	446	27.7	308	5 09NH9F	09NH9F drosophila
20	446	27.7	308	5 09VET9	09VET9 drosophila
21	444.5	27.6	479	4 08WY08	08WY08 homo sapien
22	443	27.5	482	11 09JHX4	09JHX4 ratius norv
23	425.5	26.4	538	4 08RD15	08RD15 homo sapien
24	423.5	26.3	496	4 09COK4	09COK4 homo sapien
25	414.5	25.7	399	13 091B63	091B63 xenopus lae
26	411.5	25.5	326	5 09GV88	09GV88 hydra atten
27	396	24.6	476	13 091B63	091B63 brachydanio
28	377.5	23.4	454	11 091R07	091R07 mus musculu
29	372.5	23.1	403	13 090W02	090W02 gallus gall
30	371.5	23.0	520	13 091B62	091B62 xenopus lae
31	364.5	22.6	454	11 09JHK1	09JHK1 ratius norv
32	362	22.4	500	13 091B64	091B64 xenopus lae
33	356.5	22.1	416	4 09B062	09B062 homo sapien
34	317	19.7	435	4 09BUP7	09BUP7 homo sapien
35	314.5	19.5	417	5 09Y106	09Y106 pristionchu
36	309	19.2	423	13 091B67	091B67 xenopus lae
37	305	18.9	263	5 09TZP5	09TZP5 caenorhabdi
38	305	18.9	452	11 055194	055194 ratius norv
39	305	18.9	826	5 09Y055	09Y055 caenorhabdi
40	284	17.6	268	5 09TZP6	09TZP6 caenorhabdi
41	284	17.6	536	5 018203	018203 caenorhabdi
42	275.5	17.1	393	11 09R0S9	09R0S9 mus musculu
43	255.5	15.8	450	5 09XYF4	09XYF4 drosophila
44	255	15.8	347	5 09GV89	09GV89 hydra atten
45	252	15.6	339	4 08TD13	08TD13 homo sapien

#### ALIGNMENTS

RESULT 1  
ID 088550 PRELIMINARY: PRT: 303 AA.  
AC 088550:  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE Caspase-7.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=SPLEEN;  
RA Forghani F., Roy S.;  
RT "Rat caspase-7 sequence."  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF072124; AAC24011.1;  
DR HSSP: P42574; 1PAU.  
DR MEROPS: C14.004; -.  
DR InterPro: IPR002398; ICE.  
DR InterPro: IPR002138; ICE\_P10.  
DR InterPro: IPR001309; ICE\_P20.  
DR Pfam: PF00655; ICE\_P10; 1.  
DR Pfam: PF00656; ICE\_P20; 1.  
DR PRINTS: PR00376; IILBCENZME.  
DR SMART: SMO0115; CASP. 1.  
DR PROSITE: PS01122; CASPASE\_CYS. 1.  
DR PROSITE: PS01121; CASPASE\_HIS. 1.  
DR PROSITE: PS50207; CASPASE\_P10; 1.  
DR PROSITE: PS50208; CASPASE\_P20; 1.  
SQ SEQUENCE 303 AA; A71728754BF199DD CRC64;

Query Match 86.5%; Score 1395; DB 11; Length 303;  
Best Local Similarity 84.5%; Pred. No. 1.3e-119;  
Matches 256; Conservative 21; Mismatches 26; Indels 0; Gaps 0;  
QY 1 MADQGCIEEGVDSANEDSVDAKPRSSFPVSLFSKKKNVTRISIKTRDRVPTQY 60

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Db 1 MDDDOCAAELEADSSSTEDGVADAKDRSTLISLLMKKKKNSMCPVSTTRDRVPYLY
Oy 61 NMNFEKLCIIINNNKFNKVTGMVNGDKDAEALFKCFRSLGFDVIYVNDSCAKMO 120
Db 61 RMDFEKMGCIINNNKFNKVTGMVNGDKDAEALFKCFRSLGFDVIYVNDSCAKMO 120
Oy 121 DLKKAASEBDHTNAACFACILLSHGSENVYIGKDGVTPIKDLTAHFRGDRCKTLLEKPKL 180
Db 121 DLLRRASEBDHNSACFACILLSHGSENVYIGKDGVTPIKDLTAHFRGDRCKTLLEKPKL 180
Oy 181 FFIQACRGTELDIAQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWSPGRGSM 240
Db 181 FFIQACRGTELDIAQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWSPGRGSM 240
Oy 241 FVOALCSIIIEHGKLEIMQILTRVNDVARARHFEESODDPHHEKQIOPCVSMLTRELY 300
Db 241 FVOALCSIIIEHGKLEIMQILTRVNDVARARHFEESODDPHHEKQIOPCVSMLTRELY 300
Oy 301 FSO 303
Db 301 FGR 303

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## RESULT 2

```

Oy1B65 PRELIMINARY: PRT: 318 AA.
ID 091B65
AC 091B65;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Caspase-7.
GN XCASPASE-7.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-20209426; PubMed-10744739;
RA Nakajima K., Takahashi A., Yaoita Y.;
RT "Structure, expression and function of the Xenopus laevis caspase
RT family.";
RL J. Biol. Chem. 275:10484-10491(2000).
DR EMBL; AB038170; BAA94746.1; -.
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.004; -.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_p10.
DR Pfam; PF00655; ICE_p10; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; UNKNOWN_1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SO SEQUENCE 318 AA; 35937 MW; 6EBC6684AF86A128 CRC64;

```

Query Match 63.5%; Score 1025; DB 13; Length 318;  
Best Local Similarity 65.6%; Pred. No. 1,1e-85;

Matches 196; Conservative 33; Mismatches 64; Indels 6; Gaps 2;

```

Oy 9 EEOGVEDSANDSVDAKDRSSFPVSLFSKKKNVTMRSIKT---TRDVPPTYOYNNMF 65
Db 17 DEPREEEGEDSVDAKDRSSFPVSLFSKKKNVTMRSIKT---TRDVPPTYOYNNMF 65
Oy 66 KLKGIINNNKFNKVTGMVNGDKDAEALFKCFRSLGFDVIYVNDSCAKMO 125
Db 77 NVGRCIINNNKFNKVTGMVNGDKDAEALFKCFRSLGFDVIYVNDSCAKMO 136

```

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Oy 126 ASEBDHTNAACFACILLSHGSENVYIGKDGVTPIKDLTAHFRGDRCKTLLEKPKL 185
Db 137 VAQODHDSACFACIFLSEBEGILYCTDGMPIKVLTLFRGNCISLVKPKLFLIOA 196
Oy 186 CRGTLEDIAQADSGPIND---TDANPRYKIPVEADFLFAYSTVPGYYSWSPGRGSMFV 242
Db 197 CRGHEFDGLEDAGSVNDSLETDPANRHKIPVEADFLFAYSTVPGYYSWSPGRGSMFV 256
Oy 243 QALCSIIIEHGKLEIMQILTRVNDVARARHFEESODDPHHEKQIOPCVSMLTRELY 301
Db 257 QALCSIIIEHGKLEIMQILTRVNDVARARHFEESODDPHHEKQIOPCVSMLTRELY 315

```

## RESULT 3

```

Oy98U18 PRELIMINARY: PRT: 282 AA.
ID 098U18
AC 098U18;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Caspase-3.
GN CASP3.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Yabu T., Okazaki T., Yamashita M.;
RT "Molecular Cloning and Gene Expression of Zebrafish Caspase Related to
RT Mammalian Caspase-3.";
RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB047003; BAB32409.1; -.
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.003; -.
DR ZFIN; ZDB-GENE-011210-1; casp3.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF00655; ICE_p10; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; UNKNOWN_1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SO SEQUENCE 282 AA; 31522 MW; 13C3454F5E09932E CRC64;

```

Query Match 46.2%; Score 744.5; DB 13; Length 282;  
Best Local Similarity 47.6%; Pred. No. 4,6e-60;  
Matches 147; Conservative 50; Mismatches 67; Indels 45; Gaps 5;

```

Oy 7 CIEQGVEDS-ANED-----SVDAKDRSSFPVSLFSKKKNVTMRSIKTTRDRVP 57
Db 5 CVDAKRVDYTDKSDGASASOPWQVDAKPOSHAF----- 38
Oy 58 YOYNNMFEKLCIIINNNKFNKVTGMVNGDKDAEALFKCFRSLGFDVIYVNDSCA 117
Db 39 -KSLVTPNIGACIIINNNKFNKVTGMVNGDKDAEALFKCFRSLGFDVIYVNDSCA 97
Oy 118 KMDDLKKAASEBDHTNAACFACILLSHGSENVYIGKDGVTPIKDLTAHFRGDRCKTLLEK 177
Db 98 QIMQVLTVAHDDHSCASLYCYLLSHGDEGVFEGTDSVLDKSLSLRGDRCPSLVGR 157
Oy 178 PLFPIQACRGTELDIAQADSGPINDTD---ANDPRYKIPVEADFLFAYSTVPGYYSR 233
Db 158 PLFPIQACRGTELDIPGVTD---HTDHPDIPDGERIRIPVEADFLFAYSTVPGYYSR 212
Oy 234 SPGRSMFVOALCSIIIEHGKLEIMQILTRVNDVARARHFEESODDPHHEKQIOPCVS 293
Db 213 NTMTGSWFIQSLCEKMTKIGSELELDQIMTRVNHKVALDFESTSNMPPDAKQIOPCVS 272

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QY 294 MLTKELYFS 302  
 Db 273 MLTKELYFT 281

## RESULT 4

093417 PRELIMINARY; PRT; 283 AA.  
 ID 093417  
 AC 093417  
 DT 01-NOV-1998 (TREMblrel. 08, Created)  
 DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE Caspase-3.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauvia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 NCBI\_TaxID=9031.  
 RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20149872; PubMed=10684799;  
 RA Johnson A.L., Bridgman J.T.;  
 RT "Caspase-3 and -6 expression, and enzyme activity in hen granulosa  
 cells".  
 RL Biol. Reprod. 62:589-598(2000).  
 DR EMBL: AF083029; AAC32602.1; -.  
 DR HSP; P42574; IPAU.  
 DR MEROPS: C14.003; -.  
 DR InterPro: IPR002398; ICE.  
 DR InterPro: IPR002138; ICE\_p10.  
 DR InterPro: IPR001309; ICE\_p20.  
 DR Pfam: PF00655; ICE\_p10; 1.  
 DR Pfam: PF00656; ICE\_p20; 1.  
 DR PRINTS: PRO0376; ILBCEZYME.  
 DR SMART: SM00115; CASC.1  
 DR PROSITE: PS01122; CASPASE\_CYS; 1.  
 DR PROSITE: PS01121; CASPASE\_HIS; 1.  
 DR PROSITE: PS50207; CASPASE\_P10; 1.  
 DR PROSITE: PS50208; CASPASE\_P20; 1.  
 SQ SEQUENCE 283 AA; 31675 MW; 161242DDEFDAC4F CRC64;

Query Match 46.1%; Score 743; DB 13; Length 283;  
 Best Local Similarity 52.4%; Pred. No. 6.4e-60;  
 Matches 150; Conservative 44; Mismatches 76; Indels 16; Gaps 5;

QY 17 ANDSDVAKDRSSEFVPSLSKKKKNTMRSIKTTDRV-FTYQYNNMFEKLGKCIITNN 75  
 Db 11 SGVDVSDMAC---SFGS-----KGMNLPASKSVDSGLIPDDSTRMIDYPEIGVCVIITNN 60  
 QY 76 KNFDKVTGMCVNGTGDADALFKCFRSLGPDVIVYNDSCCAKMODLLKKAASEDHNTNAA 135  
 Db 61 KNHFRDGLSSRSGTDADASVREVFMLKGLKVKTLNNDLSRODLFKLLKNNSEEDHSKRS 120  
 QY 136 CFACILLSHGEENVYKDGVTPIKDLTAHFRGDRCKTLLKPKLFITQACRGTELDLDAI 195  
 Db 121 SFYCVLLSHGDEGFLYGTGDPLELKVLTSLFRGDKRSIACKPKLFLFQACRGTELDGCI 180  
 QY 196 QASGPIINDANPRYKIPVEADFLFAYSTVPGYYSWRSRSGSPFVQALCSILEHGKELEI 255  
 Db 181 EADSGP---DETVCOKIIPVEADFLFAYSTVPGYYSWRSRSGSPFVQALCSILEHGKELEI 236  
 QY 256 LEIMQILTRVNDVRAHFESESDDPHFHEKKQIPCVVSMLEKELYF 301  
 Db 237 LEIMQILTRVNDVRAHFESESDDPHFHEKKQIPCVVSMLEKELYF 281

RESULT 5  
 096ANI PRELIMINARY; PRT; 277 AA.  
 AC 096ANI  
 DT 01-DEC-2001 (TREMblrel. 19, Created)  
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)

DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE Hypothetical 31.6 kDa protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RN  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LYMPH;  
 RA Strausberg R.;  
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC016926; AAH16926.1; -.  
 DR InterPro: IPR002398; ICE.  
 DR InterPro: IPR002138; ICE\_p10.  
 DR InterPro: IPR001309; ICE\_p20.  
 DR Pfam: PF00655; ICE\_p10; 1.  
 DR Pfam: PF00656; ICE\_p20; 1.  
 DR PRINTS: PRO0376; ILBCEZYME.  
 DR PROSITE: PS01122; CASPASE\_CYS; UNKNOWN\_1.  
 DR PROSITE: PS01121; CASPASE\_HIS; UNKNOWN\_1.  
 DR PROSITE: PS50207; CASPASE\_P10; 1.  
 DR PROSITE: PS50208; CASPASE\_P20; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 277 AA; 31608 MW; 2F35CD3BCF7FF64A CRC64;

Query Match 44.7%; Score 721; DB 4; Length 277;  
 Best Local Similarity 50.9%; Pred. No. 6.4e-58;  
 Matches 144; Conservative 50; Mismatches 77; Indels 12; Gaps 3;

QY 19 EDSVDAKDRSSEFVPSLSKKKKNTMRSIKTTDRVPTYQYNNMFEKLGKCIITNNKF 78  
 Db 5 EDSVDKSIK-NLEPKIIGSEMSDGLSDNS-----YKMDPEMGLCIITNNKF 55  
 QY 79 DKVTGMCVNGTGDADALFKCFRSLGPDVIVYNDSCCAKMODLLKKAASEDHNTNAA 138  
 Db 56 HSTGMTSRSGTDVDAANLRETFENLKYEVNRKNDLTREIYELAMDVSKEDHSKRSFV 115  
 QY 139 CILLSHGEENVYKDGVTPIKDLTAHFRGDRCKTLLKPKLFITQACRGTELDLDAIQAD 198  
 Db 116 CVLLSHGEGGILFGNGVPDLKLTINFFRGDKRSITGKPKLFIQACRGTELDGCIEND 175  
 QY 199 SGPINDTANPRYKIPVEADFLFAYSTVPGYYSWRSRSGSPFVQALCSILEHGKELEI 258  
 Db 176 SGVDVSDMAC---HKIPVADFLFAYSTVPGYYSWRSRSGSPFVQALCSILEHGKELEI 232  
 QY 259 MQLTRVNDVRAHFESESDDPHFHEKKQIPCVVSMLEKELYF 301  
 Db 233 MQLTRVNDVRAHFESESDDPHFHEKKQIPCVVSMLEKELYF 275

RESULT 6  
 095ND5 PRELIMINARY; PRT; 277 AA.  
 ID 095ND5  
 AC 095ND5  
 DT 01-DEC-2001 (TREMblrel. 19, Created)  
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
 DE Caspase-3.  
 OS Sus scrofa (pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
 NCBI\_TaxID=9823;  
 RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21334413; PubMed=11440638;  
 RA Muneta Y., Shimojima Y., Mori Y.;  
 RT "Porcine caspase-3: cloning and its activity during apoptosis of  
 porcine PK15 cells induced by porcine Fas-ligand.";  
 RL J. Interferon Cytokine Res. 21:409-415(2001).  
 DR EMBL: AB029345; BAB55544.1; -.  
 DR MEROPS: C14.003; -.  
 DR InterPro: IPR002138; ICE\_p10.  
 DR InterPro: IPR001309; ICE\_p20.



```

Db 121 ---TDEMACQKIPVADFLYAYSTARAGYSWRNSKDSMFIOSLCSMLKLYAHKLOPFMH 177
QY 261 ILTRVNDRAVRRHESQSDDPHFHEKKOIPCVVSMLTRKELF 301
Db 178 ILTRVNRKVAEFESFSLDSTFPAKKOFCIVSMLTRKELF 218

RESULT 9
ID 093415 PRELIMINARY: PRT: 304 AA.
AC 093415;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Caspase-6.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_Taxid=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20149872; PubMed-10684799;
RA Johnson A.L., Bridgham J.T.;
RT "Caspase-3 and -6 expression and enzyme activity in hen granulosa
RT cells."
RL Biol. Reprod. 62:589-598(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX PubMed-11953316;
RA Ruchaud S., Korfali N., Villa P., Kottke T.J., Dingwall C.,
RA Kaufmann S.H., Earnshaw W.C.;
RT "Caspase-6 gene disruption reveals a requirement for lamin A cleavage
RT in apoptotic chromatin condensation."
RL EMBO J. 21:1967-1977(2002).
DR EMBL: AF082329; AAC32378.1;
DR EMBL: AF469049; AAL82386.1;
DR HSSP: P42574; ICP3.
DR MEROPS: C14.005;
DR InterPro: IPR002398; ICE.
DR InterPro: IPR002138; ICE_P10.
DR InterPro: IPR001309; ICE_P20.
DR Pfam: PF00655; ICE_P10; 1.
DR Pfam: PF00656; ICE_P20; 1.
DR PRINTS: PR00376; ILBCEZYME.
DR SMART: SM00115; CASC. 1.
DR PROSITE: PS01122; CASPASE_CYS. 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
SQ SEQUENCE 304 AA; 34534 MW; 51CE31EBCAAE7383 CRC64;

Query Match 31.8%; Score 512.5; DB 13; Length 304;
Best Local Similarity 38.1%; Pred. No. 9,1e-39;
Matches 114; Conservative 51; Mismatches 113; Indels 21; Gaps 6;

QY 16 SANEDVDADKPDSSVPSLFSSKKKNVT-MRSIKTRDRVPTYYQNMNFEKLGCIITN 74
Db 9 AAGVQOLDSK-----PTTTADGNQNTTEVDAPFKRRFFDAEQYKKNHQRGVALIFN 63
QY 75 NKNPDKVTGMGRNCTDADAEALFCFRSLGFDVYIYVNDCCSAKMODLLK---ASEEDH 131
Db 64 HEHFEMRLRLDRRCOTLADRNMLKRLSLDGLFEVRIFD---LKAEDVKKVEASRDY 120
QY 132 TNACAFACILSHGEENVYIGKDGVTPIKDLTAHFRGDRCKTLLEPKRFLFIQACRGTEL 191
Db 121 SNACDFCVFLSHGENDVYIYADQIKIETITNMFGRGCKOSLVGKPKFIITIQACRGDKH 180
QY 192 DDAI-----QADSGPINDT--DANPRKIPVADFLFAYSTVPGYSWRNSPGRGSMFV 242
Db 181 DDPLVYODSVDSKRETTYNQTEVDAGVYITLPAGADFLMCISVAGGYSHRETVGSMWIT 240
QY 243 QALCSIEEHGKLEIMQILTRVNDRAVRRHESQSDDPHFHEKKOIPCVVSMLTRKELF 301

```

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Db 241 QDLCEALCKHSSLEFTELLTVNRRKVSRRYVDCRDINAIGKKOIPCFASMLTRKLYF 299

RESULT 10
ID 091866 PRELIMINARY: PRT: 303 AA.
AC 091866;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Caspase-6.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_Taxid=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20209426; PubMed-10744739;
RA Nakajima K., Takahashi A., Yeoita Y.;
RT "Structure, expression and function of the Xenopus laevis caspase
RT family."
RL J. Biol. Chem. 275:10484-10491(2000).
DR EMBL: AB038169; BAA94747.1;
DR HSSP: P42574; ICP3.
DR MEROPS: C14.005;
DR InterPro: IPR002398; ICE.
DR InterPro: IPR002138; ICE_P10.
DR InterPro: IPR001309; ICE_P20.
DR Pfam: PF00655; ICE_P10; 1.
DR Pfam: PF00656; ICE_P20; 1.
DR PRINTS: PR00376; ILBCEZYME.
DR SMART: SM00115; CASC. 1.
DR PROSITE: PS01122; CASPASE_CYS. 1.
DR PROSITE: PS01121; CASPASE_HIS. 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
SQ SEQUENCE 303 AA; 34132 MW; 4C54A0A607C69756 CRC64;

Query Match 31.6%; Score 510; DB 13; Length 303;
Best Local Similarity 37.1%; Pred. No. 1.5e-38;
Matches 108; Conservative 59; Mismatches 106; Indels 18; Gaps 4;

QY 19 EDSVDKPDSSVPSLFSSKKKNVTMRSIKTR--DRVPTYYQNMNFEKLGCIITNKK 76
Db 16 KDTSSASENK-----EOKANVTETDGMTSRTELDPESAEXYIMTKRGLALIFNHE 66
QY 77 NEDKVTGMGRNCTDADAEALFCFRSLGFDVYIYVNDCCSAKMODLLKKAASEDHNTAAC 136
Db 67 DFYQWLRLGSRGRTNTDSMLNRLILDGLFDVQNTYMLRTMDVLEKIQEASTDHSNADC 126
QY 137 FACILSHGEENVYIGKDGVTPIKDLTAHFRGDRCKTLLEPKRFLFIQACRGTELDAAI- 195
Db 127 FLCVFLSHGEDKHIYSYSLIDIQELTNPFKDGCKSLVGKPKFIITIQACRGHEHDEPVL 186
QY 196 ---QADSGP---INDTDANPRKIPVADFLFAYSTVPGYSWRNSPGRGSMFVQALCSIL 249
Db 187 KRDEVSVPLTNTTEVDASLCTLPAGADFLMCISVAGGYSHRETVGSMWYIODLCAVY 246
QY 250 EHGKLEIMQILTRVNDRAVRRHESQSDDPHFHEKKOIPCVVSMLTRKELF 300
Db 247 KAVASLEFTEILLTVNRRKVSORSVEYCDPKAIGKKOIPCFASMLTRKLF 297

RESULT 11
ID 091859 PRELIMINARY: PRT: 302 AA.
AC 091859;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Caspase 6.

```

OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Proclathopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Laling K.J., Holland J., Bonilla S., Cunningham C., Secombes C.J.;  
 RT "Cloning and sequencing of caspase 6 in rainbow trout, *Oncorhynchus*  
 RT mykiss, and analysis of its expression under conditions known to  
 RT induce apoptosis";  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF212219; AAC73848.1;  
 DR HSSP: P42574; IPAU.  
 DR MEROPS: C14.005;  
 DR InterPro: IPR002398; ICE.  
 DR InterPro: IPR002138; ICE\_P10.  
 DR InterPro: IPR001309; ICE\_P20.  
 DR Pfam: PF00655; ICE\_P10; 1.  
 DR Pfam: PF00656; ICE\_P20; 1.  
 DR PRINTS: PR00376; ILIBCENZME.  
 DR SMART: SM00115; CASC; 1.  
 DR PROSITE: PS01122; CASPASE\_CYS; 1.  
 DR PROSITE: PS01121; CASPASE\_HIS; 1.  
 DR PROSITE: PS50207; CASPASE\_P10; 1.  
 DR PROSITE: PS50208; CASPASE\_P20; 1.  
 SQ SEQUENCE 302 AA; 34082 MW; 5A6B5F28A0CFA660 CRC64;

Query Match 31.0%; Score 500.5; DB 13; Length 302;  
 Best Local Similarity 35.3%; Pred. No. 1.e-37;  
 Matches 108; Conservative 50; Mismatches 125; Indels 23; Gaps 4;

OY 3 DDOGAEIIEGVEDSANEDSVDAKPRDSSFPVSLFSSKKKKVTVRSIKTDTDPVPTGYM 62  
 DB 8 DTKGSLKXNKNTSQTGPEBNLETFDGYRCSSFSMD-----PAEYKA 51  
 OY 63 NEFKAGKCIITINNKNFDKVTGCVNGTGDADALFKCFRSLGFDVIVYVNDSCAKMQL 122  
 DB 52 NHRKRGALIFNOEHFWMHLMPPRNGTADRNGLVKRFEDLNFEVQAFNLKVEEVLQ 111  
 OY 123 LKASSEEDHTNACFACILLSHGEENVYIGKGVTPIKDLTAHFRGDRCTLLKPKLF 182  
 DB 112 ISOAAEAMNADADCFVCVSLSHGENDHYAYDKRIADITLAFKDKCKSLVKGKPRIFT 171  
 OY 183 IQACRGTELDADAIQ---ADSG-PIND--TDANPRYKIPVADFLPAYSVPGYYSWRSP 235  
 DB 172 LQACGDKRHDVTPMDVDVSEKVTNEVYVADGVYITLPAAGDFIMCYSAESYTSHRET 231  
 OY 236 GGSNFFVALCSLIEHGELEIMQILTRVNDVARRHFESOSDDPHFHEKKQIPCVSML 295  
 DB 232 INGSWYIOLCGAMKRGDSLFTTELLTLVNRKYSMRSGNCDKRAIGKKQYPCFASML 291  
 OY 296 TKELXF 301  
 DB 292 TRKLYF 297

RESULT 12  
 OY 077623 PRELIMINARY; PRT; 182 AA.  
 AC 077623;  
 DT 01-NOV-1998 (TREMblrel. 08, Created)  
 DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE Caspase-3 (Fragment).  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 OX NCBI\_TaxID=9940;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Rueda B.R., Hendry I.R., Tilly J.L., Hamernik D.L.;

RT "Accumulation of Caspase-3 mRNA and Induction of Caspase Activity in  
 RT the Ovine Corpus Luteum Following Prostaglandin-F2a Treatment in  
 RT vivo";  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF068837; AAC25713.1;  
 DR HSSP: P42574; IPAU.  
 DR MEROPS: C14.003;  
 DR InterPro: IPR002398; ICE.  
 DR InterPro: IPR002138; ICE\_P10.  
 DR InterPro: IPR001309; ICE\_P20.  
 DR Pfam: PF00655; ICE\_P10; 1.  
 DR Pfam: PF00656; ICE\_P20; 1.  
 DR PRINTS: PR00376; ILIBCENZME.  
 DR SMART: SM00115; CASC; 1.  
 DR PROSITE: PS01122; CASPASE\_CYS; 1.  
 DR PROSITE: PS01121; CASPASE\_HIS; 1.  
 DR PROSITE: PS50207; CASPASE\_P10; 1.  
 DR PROSITE: PS50208; CASPASE\_P20; 1.  
 FT NON\_TER  
 SQ SEQUENCE 182 AA; 20408 MW; B5860C6996C21BE7 CRC64;

Query Match 30.6%; Score 493.5; DB 6; Length 182;  
 Best Local Similarity 52.8%; Pred. No. 2.e-37;  
 Matches 95; Conservative 30; Mismatches 52; Indels 3; Gaps 1;

OY 60 YNNMFEKLGKCIITINNKNFDKVTGCVNGTGDADALFKCFRSLGFDVIVYVNDSCAKM 119  
 DB 6 YKNDYPMKGLCIITINNKNFHNHTGMACRSGTDVANLREFYSLKVEVRKNDLTREKEM 65  
 OY 120 QDLKASSEEDHTNACFACILLSHGEENVYIGKGVTPIKDLTAHFRGDRCTLLKPK 179  
 DB 66 LELMSDYSKEDSKRSRSEFICVLLSHGEEGIIIFGNGVDEKLLASFFRGDCRSLTGKPK 125  
 OY 180 LFLIQACRGTELDADAIDAGSPINDTDANPRYKIPVADFLPAYSVPGYYSWRSPGKS 239  
 DB 126 LFLIQACRGTELDQIETDGSSEDDMACQ--KIPVADFLYAVSTAPGYFSWNSRYGS 182

## RESULT 13

OY 099M47 PRELIMINARY; PRT; 276 AA.  
 AC 099M47;  
 DT 01-JUN-2001 (TREMblrel. 17, Created)  
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE Caspase 6.  
 GN CASP6.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC002022; AAH02022.1;  
 DR HSSP: P42574; IPAU.  
 DR MGD: MGI:1312921; Casp6.  
 DR InterPro: IPR002398; ICE.  
 DR InterPro: IPR002138; ICE\_P10.  
 DR InterPro: IPR001309; ICE\_P20.  
 DR Pfam: PF00655; ICE\_P10; 1.  
 DR Pfam: PF00656; ICE\_P20; 1.  
 DR PRINTS: PR00376; ILIBCENZME.  
 DR SMART: SM00115; CASC; 1.  
 DR PROSITE: PS01122; CASPASE\_CYS; 1.  
 DR PROSITE: PS01121; CASPASE\_HIS; 1.  
 DR PROSITE: PS50207; CASPASE\_P10; 1.  
 DR PROSITE: PS50208; CASPASE\_P20; 1.  
 SQ SEQUENCE 276 AA; 31563 MW; 5965C5932A127B6C CRC64;

Query Match 30.0%; Score 483.5; DB 11; Length 276;  
 Best Local Similarity 39.2%; Pred. No. 3.e-36;





Search completed: December 2, 2002, 12:58:10  
Job time : 29.7328 secs

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XX PF 01-NOV-1996; 96WO-US17431.
XX PR 16-NOV-1995; 95US-0558733.
XX PR 03-NOV-1995; 95US-0007211.
XX PR 06-NOV-1995; 95US-0007251.
XX PA (VERT-) VERTEX PHARM INC.
XX PI Lippke JA, Su M;
XX DR WPI; 1997-272121/24.
XX DR N-PSDB; AAT66970.
XX PT DNA encoding active, activatable or inactive cysteine protease CMH-1
XX PT - useful in gene therapy for promoting and inhibiting apoptosis and
XX PT for diagnosing cells with potential for apoptosis
XX Claim 3; Page 32-33; 48pp; English.
XX CC A proenzyme (AAW15262) is activated to CMH-1, or CPP32/Mch2
XX CC homologue-1, a human cysteine protease that is involved in
XX CC apoptosis. Its amino acid sequence was deduced from a full-length
XX CC isolated cDNA clone (AAT66970). Active, activatable (i.e. proenzyme)
XX CC or inactivated forms of CMH-1 can be expressed in prokaryotic or
XX CC eukaryotic host cells. The polypeptides are useful for screening
XX CC potential apoptosis inhibitors and for raising antibodies used to
XX CC assay CMH-1, to regulate cholesterol levels, inhibit CMH-1 activity
XX CC and therefore apoptosis, and to purify CMH-1 polypeptides.
SQ Sequence 303 AA:

Query Match 99.6%; Score 1606; DB 18; Length 303;
Best Local Similarity 99.3%; Pred. No. 1.4e-161;
Matches 301; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MADDCGIEEGVEDSANDSVDAKPRSSFPVPSLFSSKKKNVTMSIKTTTRDVRVPTQY 60
DB 1 MADDCGIEEGVEDSANDSVDAKPRSSFPVPSLFSSKKKNVTMSIKTTTRDVRVPTQY 60
QY 61 MNNEFKLGCIIINNNKNDKVTGKMGVRNGTDKDAELFCFPSLGGDVIVYNDSCAKMO 120
DB 61 MNNEFKLGCIIINNNKNDKVTGKMGVRNGTDKDAELFCFPSLGGDVIVYNDSCAKMO 120
QY 121 DLKKAASEDHHTNAACFACITLSHGEENVYIGKDGVTPIKDLTAHRRGDRCKTILEKPKL 180
DB 121 DLKKAASEDHHTNAACFACITLSHGEENVYIGKDGVTPIKDLTAHRRGDRCKTILEKPKL 180
QY 181 FFIOACRGTETLDDGIAQDSGPINDTDANPRYKIPYEADELFAVSTVPGYYSWRSRPGSGM 240
DB 181 FFIOACRGTETLDDGIAQDSGPINDTDANPRYKIPYEADELFAVSTVPGYYSWRSRPGSGM 240
QY 241 FVOALCSLIEHKGKLEIMQILTRVNDRYARHFEESODDPHHEKKQIPCVYSMLTKELY 300
DB 241 FVOALCSLIEHKGKLEIMQILTRVNDRYARHFEESODDPHHEKKQIPCVYSMLTKELY 300
QY 301 FSQ 303
DB 301 FSQ 303

RESULT 2
AAW15262
ID AAW15262 standard; Protein; 303 AA.
XX
XX AAW15262;
XX
XX 05-AUG-1997 (first entry)
XX DE Apoptotic protease Mch3-alpha.
XX Mch3-alpha; cysteine protease; apoptosis; AIDS; Ischaemia;
XX neurodegenerative disease; therapy; diagnosis.

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XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Domain 1..198
XX FT /label= P20
XX FT /note= p20 subunit
XX FT Domain 199..303
XX FT /label= p12
XX FT /note= p12 subunit
XX FT Cleavage-site 24..28
XX FT /label= P20
XX FT Cleavage-site 54..58
XX FT /label= P17
XX FT Cleavage-site 99..103
XX FT /label= P12
XX FT Active-site 184..188
XX FT /note= "QACRG active site"
XX PN W09718313-A1.
XX PD 22-MAY-1997.
XX PF 12-NOV-1996; 96WO-US18118.
XX PR 13-NOV-1995; 95US-0556627.
XX PA (IDUN-) IDUN PHARM INC.
XX PA (UYJE-) UNIV JEFFERSON THOMAS.
XX PI Alnemri ES, Armstrong R, Fernandes-Alnemri T, Litwack G;
XX PI Tomasetti K;
XX DR WPI; 1997-289289/26.
XX DR N-PSDB; AAT66992.
XX PT New gene encoding Mch3, a cysteine protease that regulates apoptosis
XX PT - for treating human diseases associated with apoptosis, and
XX PT screening for antagonists and agonists of Mch3
XX PS Claim 8; Fig 1; 52pp; English.
XX CC Human Mch3-alpha (AAW15262) is an apoptotic protein and novel member
XX CC of the interleukin-1-beta converting enzyme (ICE) family of cysteine
XX CC proteases. Its amino acid sequence was deduced from a cDNA clone
XX CC (AAT66992) obtd. from a Jurkat library. Mch3-beta (AAW15263) has also
XX CC been identified that lacks the active site of Mch3-alpha.
XX CC Mch3-alpha polypeptides can be produced in engineered host cells
XX CC and used to treat human diseases associated with cell death, such
XX CC as AIDS, ischemic injury, neurodegenerative diseases, etc. They
XX CC can also be used to regulate apoptosis and to screen for Mch3
XX CC agonists and antagonists.
SQ Sequence 303 AA:

Query Match 99.6%; Score 1606; DB 18; Length 303;
Best Local Similarity 99.3%; Pred. No. 1.4e-161;
Matches 301; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MADDCGIEEGVEDSANDSVDAKPRSSFPVPSLFSSKKKNVTMSIKTTTRDVRVPTQY 60
DB 1 MADDCGIEEGVEDSANDSVDAKPRSSFPVPSLFSSKKKNVTMSIKTTTRDVRVPTQY 60
QY 61 MNNEFKLGCIIINNNKNDKVTGKMGVRNGTDKDAELFCFPSLGGDVIVYNDSCAKMO 120
DB 61 MNNEFKLGCIIINNNKNDKVTGKMGVRNGTDKDAELFCFPSLGGDVIVYNDSCAKMO 120
QY 121 DLKKAASEDHHTNAACFACITLSHGEENVYIGKDGVTPIKDLTAHRRGDRCKTILEKPKL 180
DB 121 DLKKAASEDHHTNAACFACITLSHGEENVYIGKDGVTPIKDLTAHRRGDRCKTILEKPKL 180
QY 181 FFIOACRGTETLDDGIAQDSGPINDTDANPRYKIPYEADELFAVSTVPGYYSWRSRPGSGM 240
DB 181 FFIOACRGTETLDDGIAQDSGPINDTDANPRYKIPYEADELFAVSTVPGYYSWRSRPGSGM 240

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Db 181 FFIQACRGTELDG:IOADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSW 240  
 QY 241 FVOALCSILEEHGKLEIMQILTRVNDVARHRESQSDDPHFHEKKQIPCVSMILTREL 300  
 Db 241 FVOALCSILEEHGKLEIMQILTRVNDVARHRESQSDDPHFHEKKQIPCVSMILTREL 300  
 QY 301 FSQ 303  
 Db 301 FSQ 303

RESULT 3  
 AAY21721  
 ID AAY21721 standard; Protein; 303 AA.  
 AC AAY21721;  
 DT 10-SEP-1999 (first entry)  
 DE Amino acid sequence of caspase-7 (Mch3).  
 XX  
 XX Rev-caspase; cysteine protease; zymogen; caspase; cancer; gene therapy;  
 KM autoimmune disease; caspase-mediated apoptosis; neurodegenerative;  
 KM tumour cell; myocardial infarction; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO9935277-A2.  
 XX  
 PD 15-JUL-1999.  
 XX  
 PF 11-JAN-1999; 99WO-US00632.  
 XX  
 PR 09-JAN-1998; 98US-0070987.  
 XX  
 PA (UYJE-) UNIV JEFFERSON THOMAS.  
 XX  
 P1 Alemtet ES;  
 XX  
 DR WPI: 1999-419353/35.  
 XX  
 DR N-PSDB; AAX81223.  
 XX  
 PT New isolated nucleic acid molecule encoding a rev-caspase - used  
 PT for screening and identifying inhibitors or enhancers for treating  
 PT cancer or autoimmune disease  
 XX  
 PS Disclosure: Fig 17A-B; 74pp; English.  
 XX  
 CC The invention relates to nucleic acid molecules encoding rev-caspases.  
 CC Rev-caspases are cysteine proteases that specifically cleave proteins  
 CC after Asp residues and is expressed as a zymogen, in which the small  
 CC subunit is N-terminal to a large subunit. A gene delivery vehicle  
 CC comprising a rev-caspase coding sequence is useful for the treatment of  
 CC cancer, where the gene delivery vehicle is internalised by tumour cells.  
 CC The gene delivery vehicle can also be used to treat autoimmune diseases.  
 CC Cells transfected with a rev-caspase expressing vector can be used in  
 CC identification of inhibitors or enhancers of caspase-mediated apoptosis.  
 CC In vitro translated rev-caspase can be used to identify an inhibitor or  
 CC enhancer of caspase processing activity. Caspase inhibitors are useful  
 CC for treating neurodegenerative diseases as well as for inhibiting  
 CC apoptosis in the heart following myocardial infarction. Sequences  
 CC AAX81217-AAX81226 represent human caspase genes encoding caspase 1-10  
 CC gene products (AAY21715-Y21724).  
 XX  
 SQ Sequence 303 AA:

Query Match 99.6%; Score 1606; DB 20; Length 303;  
 Best Local Similarity 99.3%; Pred. No. 1.4e-161;  
 Matches 301; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MADDOGCIEEGVEDSANDSDVDAKDRSSFPVPSLFSKKKNVTMSIKTRRVRPTTYQ 60  
 Db 1 MADDOGCIEEGVEDSANDSDVDAKDRSSFPVPSLFSKKKNVTMSIKTRRVRPTTYQ 60

QY 61 NMNPEKIGKCIITNNKEDKVTGNGVRNGTDKDAEALFKCPRSLGPDVIYVNDSCAKMQ 120  
 Db 61 NMNPEKIGKCIITNNKEDKVTGNGVRNGTDKDAEALFKCPRSLGPDVIYVNDSCAKMQ 120  
 QY 121 DLKKASEEDHTNAACACILLSHGEENVYIGKGVPIPDLTZAHFGDRCKTLLEPKL 180  
 Db 121 DLKKASEEDHTNAACACILLSHGEENVYIGKGVPIPDLTZAHFGDRCKTLLEPKL 180  
 QY 181 FFIQACRGTELDG:IOADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSW 240  
 Db 181 FFIQACRGTELDG:IOADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSW 240  
 QY 241 FVOALCSILEEHGKLEIMQILTRVNDVARHRESQSDDPHFHEKKQIPCVSMILTREL 300  
 Db 241 FVOALCSILEEHGKLEIMQILTRVNDVARHRESQSDDPHFHEKKQIPCVSMILTREL 300  
 QY 301 FSQ 303  
 Db 301 FSQ 303

RESULT 4  
 AAE00604  
 ID AAE00604 standard; Protein; 303 AA.  
 AC AAE00604;  
 DT 02-JUL-2001 (first entry)  
 DE Human caspase-7.  
 XX  
 XX Human; caspase-7; interleukin-1 converting enzyme; ICE-LAP3; CHM-1; Mch3;  
 KM cysteine protease; apoptosis; caspase expression cassette; metastasis;  
 KM tumour; cathepsin B; urokinase; proliferation; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FT Cleavage-site 23..24  
 FT Cleavage-site /label= proteolytic\_cleavage\_site  
 FT Cleavage-site 198..199  
 FT Cleavage-site /label= proteolytic\_cleavage\_site  
 FT Cleavage-site 206..207  
 FT Cleavage-site /label= proteolytic\_cleavage\_site  
 XX  
 PN MO200129232-A2.  
 XX  
 PD 26-APR-2001.  
 XX  
 PF 19-OCT-2000; 2000WO-US28941.  
 XX  
 PR 20-OCT-1999; 99US-0160559.  
 PR 14-AUG-2000; 2000US-0225564.  
 XX  
 PA (SCIO-) SCIOS INC.  
 XX  
 PI Cordell B, Li Y;  
 XX  
 DR WPI: 2001-290920/30.  
 DR N-PSDB; AAD03914.  
 XX  
 PT Novel fusion polypeptide comprising first and second caspase subunit  
 PT separated by cleavage site not associated in nature with caspase  
 PT subunit, useful for cloning gene encoding enzymes involved in  
 PT proteolytic cleavage  
 XX  
 PS Claim 4; Fig 14; 116pp; English.  
 XX  
 CC The present amino acid sequence is human Caspase-7 also known as  
 CC interleukin-1 converting enzyme (ICE) LAP3, CHM-1 and Mch3. Caspases are  
 CC a family of cysteine proteases, that participate in the initiation and  
 CC execution of apoptosis. Caspases exist as pro-enzymes, activated by

CC cleavage into a large and small subunit, occurring after specific  
 CC aspartic acid residues within the pro-enzyme sequence.  
 CC The present invention relates to a method for functional cloning of genes  
 CC encoding proteins or enzymes involved in proteolytic cleavage. The  
 CC invention is based on the use of caspase expression cassettes comprising  
 CC the coding sequence of a proteolytic cleavage site flanked by sequences  
 CC encoding two caspase subunits. A fusion polypeptide comprising a first  
 CC and a second caspase subunit, separated by a cleavage site not associated  
 CC in nature, is useful for cloning gene encoding enzymes involved in  
 CC proteolytic cleavage. An expression cassette containing fusion  
 CC polypeptide is used to identify a mutant cell line deficient in an  
 CC enzyme of interest and is also useful for diagnosis and suppression of  
 CC proliferation or metastases of a tumour cell characterized by  
 CC overexpression of a polypeptide (e.g. Cathepsin B or urokinase,  
 CC selectively expressed in the tumour cells). DNA encoding fusion  
 CC polypeptide is used in gene therapy.  
 CC  
 SQ Sequence 303 AA;

Query Match 99.6%; Score 1606; DB 22; Length 303;  
 Best Local Similarity 99.3%; Pred. No. 1.4e-161;  
 Matches 301; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MADDGCIIEGQVEDSANEDSVDAKPPRSSFVPSLFSSKKKNVTMRISIKTRDRVPYQY 60  
 DB 1 MADDGCIIEGQVEDSANEDSVDAKPPRSSFVPSLFSSKKKNVTMRISIKTRDRVPYQY 60  
 QY 61 NMNFEKLGKCIITNNKDFKVTGMGVNNGTDKDAEALFKCFRSLGFVIVYVNDSCAKMQ 120  
 DB 61 NMNFEKLGKCIITNNKDFKVTGMGVNNGTDKDAEALFKCFRSLGFVIVYVNDSCAKMQ 120  
 QY 121 DLKKAASEDHNTAACFACILSHGEEVNYGKDGVTPIKDLTAHFGDRCKTLLEKPKL 180  
 DB 121 DLKKAASEDHNTAACFACILSHGEEVNYGKDGVTPIKDLTAHFGDRCKTLLEKPKL 180  
 QY 181 FTIOACRGTELDGIAQDSGPINDTDANPRYKIPVEADFLFAYSTVGYYSWRSPGSGSW 240  
 DB 181 FTIOACRGTELDGIAQDSGPINDTDANPRYKIPVEADFLFAYSTVGYYSWRSPGSGSW 240  
 QY 241 FVOALCSILEHKGKLEIMQILTRVNDVARHRESQSDDPHFHEKKOIPCVSMLTRELY 300  
 DB 241 FVOALCSILEHKGKLEIMQILTRVNDVARHRESQSDDPHFHEKKOIPCVSMLTRELY 300  
 QY 301 FSQ 303  
 DB 301 FSQ 303

RESULT 5  
 ABB01222  
 ID ABB01222 standard; Protein; 303 AA.  
 AC ABB01222;  
 XX  
 XX 18-SEP-2002 (first entry)  
 DE Human caspase-7 SEQ ID NO: 24.  
 DE  
 DE Human caspase-7 protein sequence SEQ ID NO:3.  
 KW Human: caspase; rev-caspase; gene therapy; protease; apoptosis;  
 KW cancer; autoimmune disease; cytostatic; immunosuppressive.  
 OS Homo sapiens.  
 OS  
 OS US6376226-B1.  
 OS  
 OS 23-APR-2002.  
 OS  
 OS 26-APR-2000; 2000US-0561756.  
 OS  
 OS 09-JAN-1998; 98US-070897P.  
 OS  
 OS 08-JAN-1999; 99US-0227721.  
 OS  
 OS (UYJE-) UNIV JEFFERSON THOMAS.

XX  
 PI Alnemri ES;  
 XX  
 XX WPI: 2002-451275/48.  
 DR N-PSDB; ABB03970.  
 XX  
 XX New rev-caspases engineered to contain the small subunit fused in frame  
 XX N-terminal to the large subunit, which is in reverse order to the wild  
 XX type caspases, are useful to treat cancer and autoimmune diseases  
 PS Disclosure; Fig 17; 81pp; English.  
 XX  
 XX The present invention provides the protein and coding sequences of human  
 XX rev-caspase-3, uncleavable rev-caspase-3 and rev-caspase-6. The sequences  
 XX can be used in the gene therapy of cancer and autoimmune diseases. The  
 XX present sequence is a protein described in the exemplification of the  
 XX invention.

Query Match 99.6%; Score 1606; DB 23; Length 303;  
 Best Local Similarity 99.3%; Pred. No. 1.4e-161;  
 Matches 301; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MADDGCIIEGQVEDSANEDSVDAKPPRSSFVPSLFSSKKKNVTMRISIKTRDRVPYQY 60  
 DB 1 MADDGCIIEGQVEDSANEDSVDAKPPRSSFVPSLFSSKKKNVTMRISIKTRDRVPYQY 60  
 QY 61 NMNFEKLGKCIITNNKDFKVTGMGVNNGTDKDAEALFKCFRSLGFVIVYVNDSCAKMQ 120  
 DB 61 NMNFEKLGKCIITNNKDFKVTGMGVNNGTDKDAEALFKCFRSLGFVIVYVNDSCAKMQ 120  
 QY 121 DLKKAASEDHNTAACFACILSHGEEVNYGKDGVTPIKDLTAHFGDRCKTLLEKPKL 180  
 DB 121 DLKKAASEDHNTAACFACILSHGEEVNYGKDGVTPIKDLTAHFGDRCKTLLEKPKL 180  
 QY 181 FTIOACRGTELDGIAQDSGPINDTDANPRYKIPVEADFLFAYSTVGYYSWRSPGSGSW 240  
 DB 181 FTIOACRGTELDGIAQDSGPINDTDANPRYKIPVEADFLFAYSTVGYYSWRSPGSGSW 240  
 QY 241 FVOALCSILEHKGKLEIMQILTRVNDVARHRESQSDDPHFHEKKOIPCVSMLTRELY 300  
 DB 241 FVOALCSILEHKGKLEIMQILTRVNDVARHRESQSDDPHFHEKKOIPCVSMLTRELY 300  
 QY 301 FSQ 303  
 DB 301 FSQ 303

RESULT 6  
 ABB09297  
 ID ABB09297 standard; Protein; 303 AA.  
 AC ABB09297;  
 XX  
 XX 15-JUL-2002 (first entry)  
 DE Human caspase 7 protein sequence SEQ ID NO:3.  
 DE  
 DE Human caspase 7 protein sequence SEQ ID NO:3.  
 KW Caspase 7; antisense modulation; antiinflammatory; cytostatic;  
 KW antisense therapy; caspase 7 inhibitor; inflammatory condition;  
 KW hyperproliferative disorder; cancer; bone metabolism; infection;  
 KW cholesterol disorder; inflammation; tumour.  
 OS Homo sapiens.  
 OS  
 OS WO200222640-A1.  
 OS  
 OS 21-MAR-2002.  
 OS  
 OS 10-SEP-2001; 2001WO-US28232.  
 OS  
 OS 11-SEP-2000; 2000US-0659860.

XX (ISIS-) ISIS PHARM INC.  
XX Zhang H, Watt AT.  
XX WPI: 2002-401902/43.  
DR N-PSDB; ABBN0825.  
XX Novel antisense compounds targeted to nucleic acids encoding caspase 7,  
PT for modulating gene expression and treating diseases associated with  
PT expression of caspase 7 in humans  
XX  
XX Example 13; Page 94-96; 138pp; English.  
XX The present invention describes a compound (I) 8-50 nucleobases in  
CC length targeted to a nucleic acid molecule encoding caspase 7, which  
CC specifically hybridises with and inhibits the expression of caspase 7.  
CC (I) has antiinflammatory and cytostatic activities, and can be used in  
CC antisense therapy and as an inhibitor of caspase 7 expression. (I) is  
CC useful for inhibiting the expression of caspase 7 in human cells or  
CC tissues, and for treating a human having a disease or condition  
CC associated with caspase 7 including inflammatory condition,  
CC hyperproliferative disorder (cancer), or bone metabolism or cholesterol  
CC disorder. (I) is useful for diagnostics, therapeutics, prophylaxis and  
CC as research reagent and kits. (I) is useful prophylactically to prevent  
CC or delay infection, inflammation or tumour formation. The present  
CC sequence represents a human caspase 7 protein, which is used in an  
CC example from the present invention.  
XX  
SQ Sequence 303 AA:  
Query Match 99.6%; Score 1606; DB 23; Length 303;  
Best Local Similarity 99.3%; Pred. No. 1.4e-161;  
Matches 301; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MADDGCIIEGVEDSANEDSVAKPDRSSVPSLFSKKKNVTMRISIKTRDRVPYQY 60  
DB 1 MADDGCIIEGVEDSANEDSVAKPDRSSVPSLFSKKKNVTMRISIKTRDRVPYQY 60  
QY 61 NMNFEKLGKCIITNNKFPDVTGNGVNRGTDKDAEALFKCRSLGFDVIVYNDSCAKMQ 120  
DB 61 NMNFEKLGKCIITNNKFPDVTGNGVNRGTDKDAEALFKCRSLGFDVIVYNDSCAKMQ 120  
QY 121 DLKKAASEEDHTNAACFACILLSHGEENVYIGKDGVTPIKDLTAHFGRDCKTLLERKPL 180  
DB 121 DLKKAASEEDHTNAACFACILLSHGEENVYIGKDGVTPIKDLTAHFGRDCKTLLERKPL 180  
QY 181 FFIQACRGTELDGDAIQADSGPINDTANPRKTIPEADFLFAYSTVPGYYSWRSPGRGSW 240  
DB 181 FFIQACRGTELDGDAIQADSGPINDTANPRKTIPEADFLFAYSTVPGYYSWRSPGRGSW 240  
QY 241 FVOALCSILIEHGKELIMQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKEYL 300  
DB 241 FVOALCSILIEHGKELIMQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKEYL 300  
QY 301 FSQ 303  
DB 301 FSQ 303  
RESULT 7  
ABB09299  
ID ABB09299 standard; Protein: 303 AA.  
XX  
AC ABB09299;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE Human caspase 7 protein sequence SEQ ID NO:17.  
XX  
KW Caspase 7; antisense modulation; antiinflammatory; cytostatic;  
KW antisense therapy; caspase 7 inhibitor; inflammation condition;  
KW hyperproliferative disorder; cancer; bone metabolism; infection;

KW Cholesterol disorder; inflammation; tumour.  
XX OS Homo sapiens.  
XX WO200222640-A1.  
XX 21-MAR-2002.  
XX 10-SEP-2001; 2001WO-0528232.  
XX 11-SEP-2000; 2000US-0659860.  
XX (ISIS-) ISIS PHARM INC.  
XX Zhang H, Watt AT;  
XX WPI: 2002-401902/43.  
DR N-PSDB; ABBN0839.  
XX Novel antisense compounds targeted to nucleic acids encoding caspase 7,  
PT for modulating gene expression and treating diseases associated with  
PT expression of caspase 7 in humans  
XX  
XX Example 15; Page 101-103; 138pp; English.  
XX The present invention describes a compound (I) 8-50 nucleobases in  
CC length targeted to a nucleic acid molecule encoding caspase 7, which  
CC specifically hybridises with and inhibits the expression of caspase 7.  
CC (I) has antiinflammatory and cytostatic activities, and can be used in  
CC antisense therapy and as an inhibitor of caspase 7 expression. (I) is  
CC useful for inhibiting the expression of caspase 7 in human cells or  
CC tissues, and for treating a human having a disease or condition  
CC associated with caspase 7 including inflammatory condition,  
CC hyperproliferative disorder (cancer), or bone metabolism or cholesterol  
CC disorder. (I) is useful for diagnostics, therapeutics, prophylaxis and  
CC as research reagent and kits. (I) is useful prophylactically to prevent  
CC or delay infection, inflammation or tumour formation. The present  
CC sequence represents a human caspase 7 protein, which is used in an  
CC example from the present invention.  
XX  
SQ Sequence 303 AA:  
Query Match 99.6%; Score 1606; DB 23; Length 303;  
Best Local Similarity 99.3%; Pred. No. 1.4e-161;  
Matches 301; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MADDGCIIEGVEDSANEDSVAKPDRSSVPSLFSKKKNVTMRISIKTRDRVPYQY 60  
DB 1 MADDGCIIEGVEDSANEDSVAKPDRSSVPSLFSKKKNVTMRISIKTRDRVPYQY 60  
QY 61 NMNFEKLGKCIITNNKFPDVTGNGVNRGTDKDAEALFKCRSLGFDVIVYNDSCAKMQ 120  
DB 61 NMNFEKLGKCIITNNKFPDVTGNGVNRGTDKDAEALFKCRSLGFDVIVYNDSCAKMQ 120  
QY 121 DLKKAASEEDHTNAACFACILLSHGEENVYIGKDGVTPIKDLTAHFGRDCKTLLERKPL 180  
DB 121 DLKKAASEEDHTNAACFACILLSHGEENVYIGKDGVTPIKDLTAHFGRDCKTLLERKPL 180  
QY 181 FFIQACRGTELDGDAIQADSGPINDTANPRKTIPEADFLFAYSTVPGYYSWRSPGRGSW 240  
DB 181 FFIQACRGTELDGDAIQADSGPINDTANPRKTIPEADFLFAYSTVPGYYSWRSPGRGSW 240  
QY 241 FVOALCSILIEHGKELIMQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKEYL 300  
DB 241 FVOALCSILIEHGKELIMQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKEYL 300  
QY 301 FSQ 303  
DB 301 FSQ 303  
RESULT 8  
ABB09300

ID ABB09300 standard; Protein; 336 AA.  
XX  
AC ABB09300;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE Human caspase 7 protein sequence SEQ ID NO:18.  
XX  
KW Caspase 7; antisense modulation; antiinflammatory; cytostatic;  
KM antisense therapy; caspase 7 inhibitor; inflammatory condition;  
KM hyperproliferative disorder; cancer; bone metabolism; infection;  
KM cholesterol disorder; inflammation; tumour.  
XX  
OS Homo sapiens.  
XX  
PN WO200222640-A1.  
XX  
PD 21-MAR-2002.  
XX  
PF 10-SEP-2001; 2001WO-US28232.  
XX  
PR 11-SEP-2000; 2000US-0659860.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Zhang H, Watt AT;  
XX  
DR WPI: 2002-401902/43.  
DR N-PSDB: ABB08040.  
XX  
PT Novel antisense compounds targeted to nucleic acids encoding caspase 7,  
PT for modulating gene expression and treating diseases associated with  
PT expression of caspase 7 in humans  
XX  
PS Example 15; Page 103-105; 138pp; English.  
XX  
XX The present invention describes a compound (I) 8-50 nucleosides in  
CC length targeted to a nucleic acid molecule encoding caspase 7, which  
CC specifically hybridises with and inhibits the expression of caspase 7.  
CC (I) has antiinflammatory and cytostatic activities, and can be used in  
CC antisense therapy and as an inhibitor of caspase 7 expression. (I) is  
CC useful for inhibiting the expression of caspase 7 in human cells or  
CC tissues, and for treating a human having a disease or condition  
CC associated with caspase 7 including inflammatory condition,  
CC hyperproliferative disorder (cancer), or bone metabolism or cholesterol  
CC disorder. (I) is useful for diagnostics, therapeutics, prophylaxis and  
CC as research reagent and kits. (I) is useful prophylactically to prevent  
CC or delay infection, inflammation or tumour formation. The present  
CC sequence represents a human caspase 7 protein, which is used in an  
CC example from the present invention.  
XX  
SQ Sequence 336 AA:  
Query Match 99.6%; Score 1606; DB 23; Length 336;  
Best Local Similarity 99.3%; Pred. No. 1.6e-161;  
Matches 301; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 241 FVOALCSILIEHGEKLEIMOLITRVNDVRVAHPESOSDDPHFRKKOIPCVSMLEKELY 300  
DB 274 FVOALCSILIEHGEKLEIMOLITRVNDVRVAHPESOSDDPHFRKKOIPCVSMLEKELY 333  
QY 301 FSO 303  
DB 334 FSO 336  
RESULT 9  
AAR95830  
ID AAR95830 standard; Protein; 341 AA.  
XX  
AC AAR95830;  
XX  
DT 28-OCT-1996 (first entry)  
XX  
DE Human interleukin-1-converting enzyme-like apoptosis protease-3.  
XX  
KW ICE-LAP-3; interleukin-1-converting enzyme-like apoptosis protease;  
KM enzyme; Alzheimer's disease; Parkinson's disease; septic shock;  
KM head injury; rheumatoid arthritis.  
XX  
OS Homo sapiens.  
XX  
PN WO9613603-A1.  
XX  
PD 09-MAY-1996.  
XX  
PF 06-JUN-1995; 95WO-US07235.  
XX  
PR 01-NOV-1994; 94US-0334251.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Hastings GA, He W, Hudson PL, Rosen CA;  
XX  
DR WPI: 1996-239509/24.  
DR N-PSDB: AAR15276.  
XX  
PT Human ICE-LAP-3 and -4 DNA and protein - useful in the diagnosis  
PT and treatment of Alzheimer's disease, Parkinson's disease,  
PT rheumatoid arthritis, septic shock and head injury  
XX  
PS Claim 1; Page 91-92; 67pp; English.  
XX  
XX This ICE-LAP-3 protein may be used therapeutically, e.g. as an  
CC antitumor or antiviral agent and to control embryonic development  
CC and tissue homeostasis. The protein can also be used to treat  
CC immunosuppression disorders, such as AIDS, by targeting virus  
CC infected cells for cell death. The DNA may find use in gene  
CC therapy applications.  
XX  
SQ Sequence 341 AA:  
Query Match 84.7%; Score 1366; DB 17; Length 341;  
Best Local Similarity 99.2%; Pred. No. 4.7e-136;  
Matches 256; Conservative 1; Mismatches 1; Indels 0; Gaps 0;



Db	260	ACRGTEFLDDGICIQADSPINDTDANPRYKILPEADFLFANSTVPGYISWSPGRGSMFVQA	319
Qy	245	LCSTLEHKGKLEIMQIL 262	
Db	320	LCSTLEHKGKLEIMQIL 337	
RESULT 10			
ID	ABM78588		
XX	ABM78588	standard; Protein; 303 AA.	
AC	ABM78588;		
XX			
DT	15-JUL-2002	(first entry)	
XX			
DE	Mouse caspase 7 protein sequence SEQ ID NO:97.		
XX			
KM	Caspase 7; antisense modulation; antiinflammatory; cytostatic;		
KM	antisense therapy; caspase 7 inhibitor; inflammatory condition;		
KM	hyperproliferative disorder; cancer; bone metabolism; infection;		
KM	cholesterol disorder; inflammation; tumour.		
XX			
OS	Mus musculus.		
XX			
PN	WO200222640-A1.		
XX			
PD	21-MAR-2002.		
XX			
PF	10-SEP-2001; 2001WO-US28232.		
XX			
PR	11-SEP-2000; 2000US-0659860.		
XX			
PA	(ISIS-) ISIS PHARM INC.		
XX			
PI	Zhang H, Watt AT;		
XX			
DR	WPI; 2002-401902/43.		
DR	N-PSDB; ABN80919.		
XX			
PT	Novel antisense compounds targeted to nucleic acids encoding caspase 7,		
PT	for modulating gene expression and treating diseases associated with		
PT	expression of caspase 7 in humans		
XX			
PS	Example 16; Page 121-123; 138pp; English.		
XX			
CC	The present invention describes a compound (I) 8-50 nucleobases in		
CC	length targeted to a nucleic acid molecule encoding caspase 7, which		
CC	specifically hybridises with and inhibits the expression of caspase 7.		
CC	(I) has antiinflammatory and cytostatic activities, and can be used in		
CC	antisense therapy and as an inhibitor of caspase 7 expression. (I) is		
CC	useful for inhibiting the expression of caspase 7 in human cells or		
CC	tissues, and for treating a human having a disease or condition		
CC	associated with caspase 7 including inflammatory condition,		
CC	hyperproliferative disorder (cancer), or bone metabolism or cholesterol		
CC	disorder. (I) is useful for diagnostics, therapeutics, prophylaxis and		
CC	as research reagent and kits. (I) is useful prophylactically to prevent		
CC	or delay infection, inflammation or tumour formation. The present		
CC	sequence represents a mouse caspase 7 protein, which is used in an		
CC	example from the present invention.		
XX			
50	Sequence 303 AA;		
Query Match	83.4%; Score 1346; DB 23; Length 303;		
Best Local Similarity	81.5%; Pred. No. 5, 2e-134;		
Matches 247; Conservative 27; Mismatches 29; Indels 0; Gaps 0			
Qy	1	MADGGCIEQGVEDSANSDESDYADPRSSFPPLSKKKKNTYMSIKTRDRVPYQY 60	
		:   :      : :   : :   :	
Db	1	MTDDQDCAALEKLVSSSDGDYADPRSSIISSILTKKRNASAGPVATGRDVPYTYL 60	
		:     :     :     :     :     :	
Qy	61	NMNFELKLCIILNKNKFDKVTGMCVRNGTDRKDAELFKCFPSLGFVIVYNDCCAKMQ 120	
		:     :     :     :     :     :	
Db	61	RMDFQKMKCIILNKNKFDKVTGMCVRNGTDRKDAELFKCFPSLGFVIVYNDCCAKMQ 120	
		:     :     :     :     :     :	

Qy	121	DLKAKASEDHRNNAACFACILLSHGSENVYKGDGTPPIKDLTAHHRGDRCKTLLEKPKL	180
Db	121	DLKRAASEDHRNNAACFACVLLSHGSEDDIYKGDGTPPIKDLTAHHRGDRCKTLLEKPKL	180
Qy	181	FTIOACRGLELDAIOADSGPINDTDANRKYKIPVADPLFAVSTVPGVYSNRSPGSGW	240
Db	181	FTIOACRGLELDDGIOADSGPINDIDANRKNKIPVADPLFAVSTVPGVYSNRNPGSGW	240
Qy	241	FVQALCSLIEHGKELEIMQILTRVNDRAVRHFEOSDDPHFEHKQKQICVYSMLTKRELY	300
Db	241	FVQALCSLIEHGKOLEIMQILTRVNDRAVRHFEOSDDPHFEHKQKQICVYSMLTKRELY	300
Qy	301	FSQ 303	
Db	301	FSR 303	
RESULT 11			
AB09298	ID	AB09298 standard; Protein; 340 AA.	
XX	AC	AB09298;	
XX	DT	15-JUL-2002 (first entry)	
DE	XX	Mouse caspase 7 protein sequence SEQ ID NO:10.	
KW	XX	Caspase 7; antisense modulation; antiinflammatory; cytosolic;	
KW	XX	antisense therapy; caspase 7 inhibitor; inflammatory condition;	
KW	XX	hyperproliferative disorder; cancer; bone metabolism; infection;	
XX	XX	cholesterol disorder; inflammation; tumour.	
OS	XX	Mus musculus.	
PN	XX	WO200222640-A1.	
PD	XX	21-MAR-2002.	
PF	XX	10-SEP-2001; 2001WO-US28232.	
PR	XX	11-SEP-2000; 2000US-0659860.	
PA	XX	(ISIS-) ISIS PHARM INC.	
PI	XX	Zhang H, Watt AT;	
DR	XX	WPI: 2002-401902/43.	
DR	XX	N-PSDB; ABN80832.	
PT	XX	Novel antisense compounds targeted to nucleic acids encoding caspase 7	
PT	XX	for modulating gene expression and treating diseases associated with	
PT	XX	expression of caspase 7 in humans	
PS	XX	Example 13; Page 97-99; 138pp; English.	
XX	XX	The present invention describes a compound (I) 8-50 nucleobases in	
XX	XX	length targeted to a nucleic acid molecule encoding caspase 7, which	
XX	XX	specifically hybridises with and inhibits the expression of caspase 7.	
XX	XX	(I) has antiinflammatory and cytostatic activities, and can be used in	
XX	XX	antisense therapy and as an inhibitor of caspase 7 expression. (I) is	
XX	XX	useful for inhibiting the expression of caspase 7 in human cells or	
XX	XX	tissues, and for treating a human having a disease or condition	
XX	XX	associated with caspase 7 including inflammatory condition,	
XX	XX	hyperproliferative disorder (cancer), or bone metabolism or cholesterol	
XX	XX	disorder. (I) is useful for diagnostics, therapeutics, prophylaxis and	
XX	XX	as research reagent and kits. (I) is useful prophylactically to prevent	
XX	XX	or delay infection, inflammation or tumour formation. The present	
XX	XX	sequence represents a mouse caspase 7 protein, which is used in an	
XX	XX	example from the present invention.	
XX	XX	Sequence 340 AA;	
XX	XX		

Query Match	83.48%	Score 1346:	DB 23:	Length 340:
Best Local Similarity	81.58%	Pred. No. 6.2e-134:		
Matches	247:	Conservative	27:	Mismatches 29; Indels 0; Gaps 0:
QY	1	MADDOGCIEEDGVESDAEDSVADAKPRDSSFFVPSLFSSKKKKVNTWRSITKTRDVPYQY	60	
Db	38	MTDDDCAAELEKEKVDSSSDGVADKPRDSSIISSIIILKKKRNASGPAVATGDRPPTLY	97	
QY	61	NNNFKLKCIIINNNKFNFKYTGWCVNRGTDKDAALFKCFRSLGFDVIVYNDSCAMQ	120	
Db	98	RMDFOKMKCIIINNNKFNFKATGMVRNGTDKDAALFKCFQNLGFEVTVHNDSCAMQ	157	
QY	121	DLTKASEEDHTNMACFCIILSHSEENVITGKDQVTPIKDLTAHFGDRCKTLLEKPKL	180	
Db	158	DLTKRASEEDHSNACFCVLLSHSEEDLIYGKDQVTPIKDLTAHFGDRCKTLLEKPKL	217	
QY	181	FFIQACRGTETLDDAIOAQSGPINDDANPRYIPEADPLFAYSVPGYYSRSPGRGSW	240	
Db	218	FFIQACRGTETLDDGIQAQSGPINDDANPRKIPPEADPLFAYSTVPGYYSWRNKGKGSW	277	
QY	241	FVOALCSITLIEHGKLEITMQILITRVNDRVARHFFESQSDPHFHEKQIIPCVASMLTKELY	300	
Db	278	FVOALCSITLIEHGKLEITMQILITRVNDSVARHFFESQSDPRENEKKIIPCVASMLTKELY	337	
QY	301	FSQ 303		
Db	338	FSR 340		

RESULT 12	
AAB98655	
ID	AAB98655 standard; protein; 244 AA.
XY	

AAC AAB98655;

DT 16-AUG-2001 (first entry)  
yy

DE Caspase-7

KM Caspase-1; Protein co-ordinate data; caspase-7; S4 binding region,  
KM Caspase-3

Not for release

XX  
DN EIC200137104-83XX  
PD 75-MAY-2001

16-NOV-2000. 2000050-1531503

XX 16-NOV-1999 0000-010000

XX  
XX  
PA (VEBT -) VEDTETV DUA DM TWO

XX  
PT      Mol v.

XX  
DR WPT: 2001-329229/3A

Molecule or molecule

PT binding pocket of caspase-7 or a homolog having an S4 binding region more hydrophilic than that of caspase-3 -

XX Example 4: Fig 3: 161ms. English

XX The present invention relates to a molecule or molecular compound (I)

comprising a binding pocket defined by the structure coordinates of caspase-7 amino acids 234, 235, 237, 276, 278, 281 and 284 or 286.

CC amino acid backbone atoms of not more than 1.5 Angstrom, where (I) b  
CC or (I) with a binding pocket having a root mean square deviation fro

present sequence is caspase-7, which was used in a sequence homology

cc alignment.  
XX

50	Sequence	244	AA;
QY	Query Match	80.8%;	Score 1304;
Db	Best Local Similarity	99.2%;	DB 22;
	Matches 242;	Conservative	1;
		Mismatches	1;
		Indels	0;
		Gaps	0;
QY	60	YNNMNEKIGKCLII	NNKNFEDKVTG
Db	1	YNNMNEKIGKCLII	NNKNFEDKVTG
QY	120	ODLLKASEEDHTNACFACILLSHGEENV	YGKGCVPIKDLTAHF
Db	61	ODLLKASEEDHTNACFACILLSHGEENV	YGKGCVPIKDLTAHF
QY	180	LFTIOACRGTELDLAIQADSGPINDTDAN	PRPKIPIVEADFLFAYSTVBP
Db	121	LFTIOACRGTELDLAIQADSGPINDTDAN	PRPKIPIVEADFLFAYSTVBP
QY	240	WFVQALCSITEEHGKELEIMQILTRVND	RVARHFEESQSDDPHFHEKKOIPC
Db	181	WFVQALCSITEEHGKELEIMQILTRVND	RVARHFEESQSDDPHFHEKKOIPC
QY	300	YFSQ	303
Db	241	YFSQ	244

RESULT 13  
AAW15263

ID	AAW15263	standard; protein; 253 AA.
XX		

XX  
XX

DI 03-AUG-1991 (FIRST ENTRY)  
XX

cysteine protease mcrs beta-  
XX  
XX

KW neurodegenerative disease; therapy; diagnosis.

05 Homo sapiens.

Key	Location/Qualifiers
FH	

```

11 coverage size 24:120
Et /label= p20

```

	/label= P17
FT	

PN W09718313-A1.

PD 22-MAY-1997.

PF 12-NOV-1996; 96WO-US18118.

PR 13-NOV-1995; 95US-0556627.

PA (IDUN-) IDUN PHARM INC.

XX  
XX

PI Tomasek K;

DR WPI; 1997-289289/26.

[illegible]

PT - for treating human diseases associated with apoptosis, and searching for natural products associated with apoptosis.

XX C]ajm 8: Efr 1: 53m: Enaj:ch  
DS

Human Mcb3-beta (AA115363) is a member of the histone subfamily 3

CC beta converting enzyme (ICE) family of cysteine proteases. Its

CC amino acid sequence was deduced from a cDNA clone (AA66993) obtd.  
 CC from a Jurkat library. Mch3-beta mRNA arises from 2 simultaneous  
 CC alternative splicing events that result in a shift in the reading  
 CC frame after amino acid 148 of Mch3-alpha (AAW15262). Mch3-beta does  
 CC not include the QACRG active site pentapeptide sequence of  
 CC Mch3-alpha. Mch3-beta polypeptides can be produced in engineered  
 CC host cells. They can be used as dominant/negative inhibitors of  
 CC apoptotic Mch3-alpha to treat or reduce the severity of diseases  
 CC characterised by increased programmed cell death, such as AIDS,  
 CC ischemic injury, neurodegenerative diseases, etc., and can also  
 CC be used to screen for Mch3 agonists and antagonists.

SO Sequence 253 AA;

Query Match 48.6%; Score 783.5; DB 18; Length 253;  
 Best Local Similarity 99.3%; Pred. No. 1.9e-74;  
 Matches 148; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADDOGCEEGVEDSANEVDKAPDRSSFPSPSLFSSKKKKVTKRSIKTTDRVPPTYQ 60  
 DB 1 MADDOGCEEGVEDSANEVDKAPDRSSFPSPSLFSSKKKKVTKRSIKTTDRVPPTYQ 60  
 QY 61 NMNFEKLGKCIILNNKNFDKVTGKVGNGTGDKADEALFKCFRSLGFDVIYVNDSCAKMQ 120  
 DB 61 NMNFEKLGKCIILNNKNFDKVTGKVGNGTGDKADEALFKCFRSLGFDVIYVNDSCAKMQ 120  
 QY 121 DLKKASEEDHTNACFACILLSHGEENV 149  
 DB 121 DLKKASEEDHTNACFACILLSHGEENV 149

#### RESULT 14

ID ABB78587 standard; Protein; 253 AA.

AC ABB78587;

DT 15-JUL-2002 (first entry)

DE Human caspase 7 protein sequence SEQ ID NO:19.

KW Caspase 7; antisense modulation; antiinflammatory; cytostatic;  
 KW antisense therapy; caspase 7 inhibitor; inflammatory condition;  
 KW hyperproliferative disorder; cancer; bone metabolism; infection;  
 KW cholesterol disorder; inflammation; tumour.

OS Homo sapiens.

PN WO200222640-A1.

PD 21-MAR-2002.

PF 10-SEP-2001; 2001WO-US28232.

PR 11-SEP-2000; 2000US-0659860.

PA (ISIS-) ISIS PHARM INC.

PI Zhang H, Watt AT;

PI MPI; 2002-401902/43.

DR N-PSDB; ABRN0841.

PT Novel antisense compounds targeted to nucleic acids encoding caspase 7,  
 PT for modulating gene expression and treating diseases associated with  
 PT expression of caspase 7 in humans

PS Example 15; Page 105-107; 138pp; English.

CC The present invention describes a compound (I) 8-50 nucleobases in  
 CC length targeted to a nucleic acid molecule encoding caspase 7, which  
 CC specifically hybridises with and inhibits the expression of caspase 7.  
 CC (I) has antiinflammatory and cytostatic activities, and can be used in

CC antisense therapy and as an inhibitor of caspase 7 expression. (I) is  
 CC useful for inhibiting the expression of caspase 7 in human cells or  
 CC tissues, and for treating a human having a disease or condition  
 CC associated with caspase 7 including inflammatory condition,  
 CC hyperproliferative disorder (cancer), or bone metabolism or cholesterol  
 CC disorder. (I) is useful for diagnostics, therapeutics, prophylaxis and  
 CC as research reagent and kits. (I) is useful prophylactically to prevent  
 CC or delay infection, inflammation or tumour formation. The present  
 CC sequence represents a human caspase 7 protein, which is used in an  
 CC example from the present invention.

SO Sequence 253 AA;

Query Match 48.6%; Score 783.5; DB 23; Length 253;  
 Best Local Similarity 99.3%; Pred. No. 1.9e-74;  
 Matches 148; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADDOGCEEGVEDSANEVDKAPDRSSFPSPSLFSSKKKKVTKRSIKTTDRVPPTYQ 60  
 DB 1 MADDOGCEEGVEDSANEVDKAPDRSSFPSPSLFSSKKKKVTKRSIKTTDRVPPTYQ 60  
 QY 61 NMNFEKLGKCIILNNKNFDKVTGKVGNGTGDKADEALFKCFRSLGFDVIYVNDSCAKMQ 120  
 DB 61 NMNFEKLGKCIILNNKNFDKVTGKVGNGTGDKADEALFKCFRSLGFDVIYVNDSCAKMQ 120  
 QY 121 DLKKASEEDHTNACFACILLSHGEENV 149  
 DB 121 DLKKASEEDHTNACFACILLSHGEENV 149

#### RESULT 15

ID AAW00372 standard; protein; 277 AA.

AC AAW00372;

DT 26-JUN-1997 (first entry)

DE Apopain CPP32beta proenzyme.

KW CPP32beta; isoform; inactive; CPP32; proenzyme; cysteine; protease;  
 KW proteolytic product; poly(DP-ribose) polymerase; PARP; apopain;  
 KW cleavage enzyme; human; monocytic leukemia; cell line; THP-1;  
 KW identification; modulator; recombinant production; gene therapy;  
 KW pro-inflammatory; pro-apoptotic; apoptosis; inflammation; antibody;  
 KW antisense DNA; treatment; immune; proliferation; degeneration;  
 KW disease; AIDS; acquired immunodeficiency syndrome; autoimmune;  
 KW pathogenic infection; cardiovascular; neurological; injury;  
 KW alopecia; ageing; cancer; type I diabetes; Parkinson's;  
 KW Alzheimer's.

OS Homo sapiens.

PN Key Location/Qualifiers

FT Domain 1..28 /note= "amino-terminal pro-domain"

FT Cleavage-site 28..29

FT Region 29..46 /note= "amino-terminal sequence determined for

FT Protein 29..175 /note= "17 kDa subunit p17"

FT Cleavage-site 175..176

FT Region 176..193 /note= "amino-terminal sequence determined for

FT Region 161..165 /note= "conserved pentapeptide containing putative

FT Protein 176..277 /note= "catalytic cysteine"

PN WO9633268-A1.

XX 24-OCT-1996.  
 PD  
 XX  
 PF 17-APR-1996; 96MO-US05282;  
 XX  
 PR 21-APR-1995; 95US-0426557.  
 XX  
 PA (MERI ) MERCK & CO INC.  
 XX (MERI ) MERCK FROSST CANADA INC.  
 XX  
 PI Ali A, Miller DK, Nicholson DW, Thornberry NA, Vaillancourt JP;  
 XX WPI: 1996-485775/48.  
 DR  
 XX  
 PT Apopain, a new human apoptosis related enzyme - responsible for the  
 PT proteolytic breakdown of poly(ADP-ribose) polymerase (PARP) which  
 PT occurs at the onset of apoptosis  
 XX  
 PS Claim 1; Fig 4C; 84pp; English.  
 XX  
 CC The present sequence is the CPP32beta or Glu190 isoform of the  
 CC inactive CPP32 proenzyme (a member of the interleukin converting  
 CC enzyme/pro-apoptotic protein CED-3 family of cysteine proteases of  
 CC unknown function cloned from Jurkat cells), the proteolytic product  
 CC of which is the poly(ADP-ribose) polymerase (PARP) protease.  
 CC Apopain. The PARP cleavage enzyme was purified from the human  
 CC monocytic leukaemia cell line, THP-1, using standard ion exchange  
 CC chromatography techniques and SDS PAGE. Apopain can be used to  
 CC identify apopain activity modulators, while apopain encoding DNA  
 CC may be used for apopain production or in gene therapy (i.e. in vivo  
 CC or ex vivo gene transplantation) for enhancing the pro-inflammatory  
 CC or pro-apoptotic effects of apopain. Anti-apopain antibodies and  
 CC antisense DNA can be used to reduce or eliminate the  
 CC pro-inflammatory or pro-apoptotic effects of apopain. Modulation  
 CC of apopain activity is beneficial in the treatment of immune,  
 CC proliferative and degenerative diseases, e.g. AIDS, autoimmune  
 CC disease, pathogenic infections, cardiovascular and neurological  
 CC injury, alopecia, ageing, cancer, type I diabetes and Parkinson's  
 CC and Alzheimer's disease.  
 CC  
 XX  
 SQ Sequence 277 AA;  
 Query Match 44.7%; Score 721; DB 17; Length 277;  
 Best Local Similarity 50.9%; Pred No. 9, 1e-68;  
 Matches 144; Conservative 50; Mismatches 77; Indels 12; Gaps 3;  
 OY 19 EDSVDKPPDRSSFFVPSLFSKRRKNTMRSIKTRDRVPTVYQNMNFEKLGKCIINNNKF 78  
 DB 5 ENSVDSKSIK-NLEPKRIHSGESMDSGISLDS-----YKMDYFEMGLCIIINNNKF 55  
 OY 79 DKVTGMGVANGTDKDAEALFKCFRSLGFDVYIYNDSCAKMODLTKASEDHTNAACFA 138  
 DB 56 HKSTGTSKSGTDVAANLRETFRNLYEVNRKNDLTREIYELMRDVSKEHSSKSSFY 115  
 OY 139 CILSHGEENVYIKGDTVPIDLTAFHGRDCKTILEKPKLFIOACRSTELDAIQAD 198  
 DB 116 CVLLSHGEGGILFGTNGPVLDLKKITNEFRGDRCLTGRPKLFIQACRTELDGIFTD 175  
 OY 199 SGPINDTANPRKIPVEADFLFAYSTVGYYSWRSPRGSMFVQALCSILIEHGKELET 258  
 DB 176 SGVDDDMAC---HKIPVEADFLFAYSTVGYYSWRSPRGSMFVQALCSILIEHGKELET 258  
 OY 259 MOILTRVNDVARHFEESQSDPHFHEKKOIPCVMSLTKELVF 301  
 DB 233 MHILTRVNRKVKATEFEESFSFDATFPAKKOIPCIVSMLTKELVF 275

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 2, 2002, 12:57:12 : Search time 8.35862 Seconds  
(Without alignments)  
577.252 Million cell updates/sec

Title: US-09-895-263-2

Perfect score: 1613  
Sequence: 1 MADDCGIEGVEDSANED.....EKKQIPCVSMLEKLYFSQ 303

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 102317 seqs, 15924203 residues

Total number of hits satisfying chosen parameters: 102317

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published\_Applications\_AA: \*  
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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB pep: \*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB pep: \*  
4: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB pep: \*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB pep: \*  
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14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1606	99.6	303	10	US-09-944-851-2
3	1606	99.6	303	10	US-09-954-697-24
4	721	44.7	277	10	US-09-895-263-4
5	718	44.5	277	10	US-09-954-697-12
6	716.5	44.4	264	9	US-10-103-448-3
7	474	29.4	293	10	US-09-954-697-21
8	444.5	27.6	479	10	US-09-952-768-2
9	444.5	27.6	479	10	US-09-954-697-33
10	425.5	26.4	479	10	US-09-410-194-20
11	425.5	26.4	571	10	US-09-410-194-21
12	423.5	26.3	286	10	US-09-862-915-1
13	423.5	26.3	496	10	US-09-952-768-4
14	420.5	26.1	476	10	US-09-954-697-27
15	395	24.5	521	10	US-09-962-834A-2
16	389	24.1	290	10	US-09-954-697-34
17	387	24.0	285	10	US-09-954-697-35
18	372	23.1	503	10	US-09-888-243-29
19	370	22.9	505	10	US-09-888-243-5

20	357.5	22.2	479	10	US-09-888-243-6	Sequence 6, Appli
21	356.5	22.1	416	9	US-10-068-569-1	Sequence 1, Appli
22	347.5	21.5	416	10	US-09-954-697-30	Sequence 30, Appli
23	342	21.2	354	10	US-09-888-243-20	Sequence 2, Appli
24	342	21.2	503	10	US-09-888-243-2	Sequence 2, Appli
25	332.5	20.6	182	10	US-09-809-905-2	Sequence 2, Appli
26	321.5	19.9	167	10	US-09-864-761-48728	Sequence 48728, A
27	317	19.7	435	10	US-09-954-697-9	Sequence 9, Appli
28	308	19.1	451	10	US-09-888-243-28	Sequence 28, Appli
29	300	18.6	163	10	US-09-864-761-47950	Sequence 47950, A
30	264	16.4	52	10	US-09-989-903-40	Sequence 40, Appli
31	264	16.4	81	10	US-09-989-903-35	Sequence 35, Appli
32	263	16.3	300	10	US-09-954-697-36	Sequence 36, Appli
33	258	16.0	242	10	US-09-764-803A-24	Sequence 24, Appli
34	258	16.0	242	10	US-09-845-028-9	Sequence 9, Appli
35	255	15.8	242	10	US-09-845-028-2	Sequence 2, Appli
36	252	15.6	229	10	US-09-764-803A-4	Sequence 4, Appli
37	252	15.6	242	10	US-09-989-903-5	Sequence 5, Appli
38	251.5	15.6	257	10	US-09-764-803A-2	Sequence 2, Appli
39	251.5	15.6	260	10	US-09-989-903-2	Sequence 2, Appli
40	241	14.9	51	10	US-09-989-903-41	Sequence 41, Appli
41	224.5	13.9	410	10	US-09-917-265-24	Sequence 24, Appli
42	221.5	13.7	410	10	US-09-917-265-15	Sequence 15, Appli
43	210	13.0	47	10	US-09-989-903-36	Sequence 36, Appli
44	210	13.0	418	10	US-09-954-697-18	Sequence 18, Appli
45	209	13.0	214	10	US-09-989-903-9	Sequence 9, Appli

#### ALIGNMENTS

RESULT 1  
US-09-895-263-2  
Sequence 2, Application US/09895263  
Patent No. US20020076793A1  
GENERAL INFORMATION:  
APPLICANT: He, Wei-Wu et al.  
TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme  
like Apoptosis Protease 3 and 4  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Ave.  
CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/895,263  
FILING DATE: 02-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: <Unknown>  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Jonathan L. Klein  
REGISTRATION NUMBER: 41,119  
REFERENCE/DOCKET NUMBER: PFI40  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-251-6015  
TELEFAX: 301-309-8439  
INFORMATION FOR SEQ ID NO. 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 303 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein

Db 1 MADDGCIIEGVEDSANDSDVAKPDRSSFVPSLFSSKKKNVTMRSIKTTDRVPTYQ 60  
Qy 61 NMNFKLGKCIITNNKNDKVTGKVGRTGDKDALEKCRSLGFDVIYVNDSCAKM 120  
Db 61 NMNFKLGKCIITNNKNDKVTGKVGRTGDKDALEKCRSLGFDVIYVNDSCAKM 120  
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Db 121 DLTKASEEDHTNACFACILSHGEENVYIGKGVPTIKDLTAHFRDRCCTLLEKPKL 180  
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Db 181 FFIQACRGTELDIAIQADSGPINDTDANPRYKIPVEADFLAYSTVPYYSMRSPGRGSW 240  
Qy 241 FVQALCSILEBHGKLEIMQILTRVNDVRAHFEQSODDPHFHEKKQIPCVVSMLTKEYL 300  
Db 241 FVQALCSILEBHGKLEIMQILTRVNDVRAHFEQSODDPHFHEKKQIPCVVSMLTKEYL 300  
Qy 301 FSQ 303  
Db 301 FSQ 303

## RESULT 2

US-09-561-756-24  
Sequence 24, Application US/09561756  
Patent No. 6376226  
GENERAL INFORMATION:  
APPLICANT: Alnemrl, Emad S.  
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES  
FILE REFERENCE: 480140.431  
CURRENT APPLICATION NUMBER: US/09/561,756  
CURRENT FILING DATE: 2000-04-26  
PRIOR APPLICATION NUMBER: 09/227,721  
PRIOR FILING DATE: 1999-01-08  
NUMBER OF SEQ ID NOS: 116  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 24  
LENGTH: 303  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-561-756-24

Query Match 99.6%; Score 1606; DB 4; Length 303;  
Best Local Similarity 99.3%; Pred. No. 6.4e-174;  
Matches 301; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MADDGCIIEGVEDSANDSDVAKPDRSSFVPSLFSSKKKNVTMRSIKTTDRVPTYQ 60  
Db 1 MADDGCIIEGVEDSANDSDVAKPDRSSFVPSLFSSKKKNVTMRSIKTTDRVPTYQ 60  
Qy 61 NMNFKLGKCIITNNKNDKVTGKVGRTGDKDALEKCRSLGFDVIYVNDSCAKM 120  
Db 61 NMNFKLGKCIITNNKNDKVTGKVGRTGDKDALEKCRSLGFDVIYVNDSCAKM 120  
Qy 121 DLTKASEEDHTNACFACILSHGEENVYIGKGVPTIKDLTAHFRDRCCTLLEKPKL 180  
Db 121 DLTKASEEDHTNACFACILSHGEENVYIGKGVPTIKDLTAHFRDRCCTLLEKPKL 180  
Qy 181 FFIQACRGTELDIAIQADSGPINDTDANPRYKIPVEADFLAYSTVPYYSMRSPGRGSW 240  
Db 181 FFIQACRGTELDIAIQADSGPINDTDANPRYKIPVEADFLAYSTVPYYSMRSPGRGSW 240  
Qy 241 FVQALCSILEBHGKLEIMQILTRVNDVRAHFEQSODDPHFHEKKQIPCVVSMLTKEYL 300  
Db 241 FVQALCSILEBHGKLEIMQILTRVNDVRAHFEQSODDPHFHEKKQIPCVVSMLTKEYL 300  
Qy 301 FSQ 303  
Db 301 FSQ 303

RESULT 3  
US-09-227-721-24  
Sequence 24, Application US/09227721  
Patent No. 6379950  
GENERAL INFORMATION:  
APPLICANT: Alnemrl, Emad S.  
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES  
FILE REFERENCE: 480140.431  
CURRENT APPLICATION NUMBER: US/09/227,721  
CURRENT FILING DATE: 1999-01-08  
NUMBER OF SEQ ID NOS: 116  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 24  
LENGTH: 303  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-227-721-24

Query Match 99.6%; Score 1606; DB 4; Length 303;  
Best Local Similarity 99.3%; Pred. No. 6.4e-174;  
Matches 301; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MADDGCIIEGVEDSANDSDVAKPDRSSFVPSLFSSKKKNVTMRSIKTTDRVPTYQ 60  
Db 1 MADDGCIIEGVEDSANDSDVAKPDRSSFVPSLFSSKKKNVTMRSIKTTDRVPTYQ 60  
Qy 61 NMNFKLGKCIITNNKNDKVTGKVGRTGDKDALEKCRSLGFDVIYVNDSCAKM 120  
Db 61 NMNFKLGKCIITNNKNDKVTGKVGRTGDKDALEKCRSLGFDVIYVNDSCAKM 120  
Qy 121 DLTKASEEDHTNACFACILSHGEENVYIGKGVPTIKDLTAHFRDRCCTLLEKPKL 180  
Db 121 DLTKASEEDHTNACFACILSHGEENVYIGKGVPTIKDLTAHFRDRCCTLLEKPKL 180  
Qy 181 FFIQACRGTELDIAIQADSGPINDTDANPRYKIPVEADFLAYSTVPYYSMRSPGRGSW 240  
Db 181 FFIQACRGTELDIAIQADSGPINDTDANPRYKIPVEADFLAYSTVPYYSMRSPGRGSW 240  
Qy 241 FVQALCSILEBHGKLEIMQILTRVNDVRAHFEQSODDPHFHEKKQIPCVVSMLTKEYL 300  
Db 241 FVQALCSILEBHGKLEIMQILTRVNDVRAHFEQSODDPHFHEKKQIPCVVSMLTKEYL 300  
Qy 301 FSQ 303  
Db 301 FSQ 303

RESULT 4  
US-08-556-627A-2  
Sequence 2, Application US/08556627A  
Patent No. 6462175  
GENERAL INFORMATION:  
APPLICANT: Alnemrl, Emad S.  
APPLICANT: Fernandes-Alnemrl, Teresa  
APPLICANT: Litwack, Gerald  
APPLICANT: Armstrong, Robert  
APPLICANT: Tomaselli, Kevin  
TITLE OF INVENTION: Mch3, A No. 6462175e1 Apoptotic Protease,  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

Db	181	FFIOACRGELDDG:IGADGSP:INDNDANPRYILPEADFLFAYSTVPGYYSMRSPRGSM	240
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Db	241	FVALCSLIEEHGKLEIMQILTRVNDRYARHFEQSDDPHFEKKQIPCVYSMLTKELY	300
Qy	301	FSQ 303	
Db	301	FSQ 303	
RESULT 4			
US-09-895-263-4			
Sequence 4, Application US/09895263			
Patent No. US20020076793A1			
GENERAL INFORMATION:			
APPLICANT: He, Wei-Wu et al.			
TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme			
Like Apoptosis Protease 3 and 4			
NUMBER OF SEQUENCES: 12			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Human Genome Sciences, Inc.			
STREET: 9410 Key West Ave.			
CITY: Rockville			
STATE: MD			
COUNTRY: USA			
ZIP: 20850			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: PatentIn Release #1.0, Version #1.30			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/09/895,263			
FILING DATE: 02-Jul-2001			
CLASSIFICATION: <Unknown>			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: <Unknown>			
FILING DATE: <Unknown>			
ATTORNEY/AGENT INFORMATION:			
NAME: Jonathan L. Klein			
REGISTRATION NUMBER: 41,119			
REFERENCE/DOCKET NUMBER: PFI40			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: 301-251-6015			
TELEFAX: 301-309-8439			
INFORMATION FOR SEQ ID NO: 4:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 277 amino acids			
TYPE: amino acid			
STRANDEDNESS: single			
TOPOLOGY: linear			
MOLECULE TYPE: protein			
SEQUENCE DESCRIPTION: SEQ ID NO: 4:			
US-09-895-263-4			
Query Match			
Best local similarity 44.7%; Score 721; DB 10; Length 277;			
Matches 144; Conservative 50; Mismatches 77; Indels 12; Gaps 3;			
Qy	19	EDSVADKPRDSFVSLSPSKKKKNTTMRSIKTRRVRVPTYYQYNNFELGKCIINNNKF	78
Db	5	ENSVDSKSIK-NLEPKIIHGSSEMSDGSIDNS-----YKMDYPEMGLCIITNNKF	55
Qy	79	DKYVGMGVRNGTDKAELALFCFSLGSDVIYINDCSCAKMODLLKASEDHTNAACFA	138
Db	56	HKSTGMRSGTDVAANLRETFRNLKYEVRNKNDLTREIYELMRDYSKEDHSKRSPV	115
Qy	139	CIILSHGSENYVYGKGVTPIKDLTAHFRGDRCKTLLEPKPLFTIOACRGTELDIAIOD	198
Db	116	CVLLSHGEGEIIIFGNGRPVDLKKIINFRGDCRSILTGKPKLFTIOACRGTELDGCIETD	175
Qy	199	SGPIINDTANPRYIKVEADFLFAYSTVPGYYSMRSPRGSMFVALCSLIEEHGKLEI	258

[illegible]

TELEFAX: 301-309-8439  
; INFORMATION FOR SEQ ID NO: 4:

NAME: DURETTE, PHILIPPE L.  
REGISTRATION NUMBER: 35 125

REFERENCE/DOCKET NUMBER: 19824Y



[illegible]

```

; SEQ ID NO 20
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-410-194-20

Query Match                26.4%; Score 425.5; DB 10; Length 479;
Best Local Similarity      35.4%; Pred. No. 1,4e-35;
Matches 112; Conservative 49; Mismatches 114; Indels 41; Gaps 10

QY   EGVGVDSANEDSVDAKPPRSSFPVSLFSKKKNVTMR--SIKTTRDRVPTRYQMNF 65
DB   179 EEFSKRSS---SLESPPDFSGEELCGVMITSDSPRODDSFQSÜTLDKV----YMKSR 231
QY   KLGKCIINNNKF-----DKVTGMGVNGTGDKADEALFKGRSLGFVIYVNDSCAK 118
DB   232 PGYCIIINNHNPAKAREKVPKLHSIRDNONGTHLDAGALLTFTEELHFEIKRPHDCTVQ 291
QY   119 MODLLKASSEDHTNACACILSHGENNVYIGKD-VTPIKDLTAHRGDRCKTLLEK 177
DB   292 IYEILKIYOLMHNSMNDCCICILSHGDKGIYGTDGGAPEIYELISOPTGLKPSLACK 351
QY   178 PLKFIIOACRGTELDAIDADSPINDTANP-----RYKIPAEADFIFYSTV 226
DB   352 PVVFIIQACGGONYOKGIVET---DSEQPYLEMDLSSPOTRY-IDPADFLGMATV 406
QY   227 PSYVSRSFGRSWFMFOALCSILEEH-GKELEIMQITFRVNDRVARHFESQSDDPFHFK 285
DB   407 NNCVCYSRNPAEGTVTIQSLCQSLRENCPRGDDILTILTEVN-----YEVSKDKKKNMG 460
QY   286 KOIPCYSMLTKELYF 301
DB   461 KQMPQPTFLRKLYE 476

RESULT 11
US-09-410-194-21
; Sequence 21, Application US/09410194
; Patent No. US20020095030A1
; GENERAL INFORMATION:
; APPLICANT : Tschopp, Jurg
; APPLICANT : Thome, Margot
; APPLICANT : Burns, Kimberly
; APPLICANT : Imbler, Marten
; APPLICANT : Hahne, Michael
; APPLICANT : Schroter, Michael
; APPLICANT : Schneider, Pascal
; APPLICANT : Bodmer, Jean-Luc
; APPLICANT : Steiner, Veronique
; APPLICANT : Rimoldi, Donata
; APPLICANT : Hofmann, Kay
; APPLICANT : French, E. Lars
; TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
; FILE REFERENCE: 11141-002001
; CURRENT APPLICATION NUMBER: US/09/410.194
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/EP98/01857
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-410-194-21

Query Match                26.4%; Score 425.5; DB 10; Length 571;
Best Local Similarity      29.9%; Pred. No. 1,7e-35;
Matches 109; Conservative 61; Mismatches 110; Indels 85; Gaps 11;

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Db 116 CULLSHGEEGIIFGTNGPVLKKTITNFRGDRCSLTGKPKLFIIOACRGTELDGCIETD 175  
QY 199 SGPINDTDANPRKPIPEADFLFAFSTVPGYYSRSPGSGMFVQALCSILEHCKELEI 258  
Db 176 SGVDDMAC--HKIPVADDFLVAYSTAPGYYSRNSKDSGFWFQSLCAMLKQYADKLEF 232  
QY 259 MQLITRVNDRVARHFESQSDPHHEKKQIPCVVSMLTKELYF 301  
Db 233 MHLITRVNKRKVAEFESFSDATFPAKQIPCIIVSMLTKELYF 275

## RESULT 11

US-09-227-721-12  
Sequence 12, Application US/09227721  
Patent No. 6379950  
GENERAL INFORMATION:  
APPLICANT: Alnemrl, Emaad S.  
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES  
FILE REFERENCE: 480140.431  
CURRENT APPLICATION NUMBER: US/09/227,721  
CURRENT FILING DATE: 1999-01-08  
NUMBER OF SEQ ID NOS: 116  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 12  
LENGTH: 277  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-227-721-12

Query Match 44.5%; Score 718; DB 4; Length 277;  
Best Local Similarity 50.5%; Pred. No. 3.5e-73;  
Matches 143; Conservative 51; Mismatches 77; Indels 12; Gaps 3;

QY 19 EDSVDKPRDSSVPSLFSKSKKKVNTKRTDRVPTVQYNNFELGKCIINKNF 78  
Db 5 ENSVDSKIR-NLEPKIIHGESMDSGISLDNS-----YKMDYPEMGICIIINKNF 55  
QY 79 DKYTGKGVNRGTGDAEALFKCFRSLGFDYIVYNDSCAKMODILKKAASEDHNAACFA 138  
Db 56 HKSTGMSRSGTDVDANLRETFRNKLYEVNKNNDLREIVELMRVSKEDHSKRSSFV 115  
QY 139 CILLSHGEENVYIGKDVPTPIKDLTAHFRGDRCKTLLEKPKLFIOACRGTELDLDAIOAD 198  
Db 116 CULLSHGEEGIIFGTNGPVLKKTITNFRGDRCSLTGKPKLFIIOACRGTELDGCIETD 175  
QY 199 SGPINDTDANPRKPIPEADFLFAFSTVPGYYSRSPGSGMFVQALCSILEHCKELEI 258  
Db 176 SGVDDMAC--HKIPVADDFLVAYSTAPGYYSRNSKDSGFWFQSLCAMLKQYADKLEF 232  
QY 259 MQLITRVNDRVARHFESQSDPHHEKKQIPCVVSMLTKELYF 301  
Db 233 MHLITRVNKRKVAEFESFSDATFPAKQIPCIIVSMLTKELYF 275

## RESULT 12

US-08-983-502-30  
Sequence 30, Application US/08983502  
Patent No. 6399327  
GENERAL INFORMATION:  
APPLICANT: David WALLACH  
APPLICANT: Mark P. BOLDIN  
APPLICANT: Tanya M. GONCHAROV  
APPLICANT: Yury V. GOLTSEV  
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS  
TITLE OF INVENTION: AND OTHER PROTEINS  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Browdy and Neimark  
STREET: 419 Seventh Street N.W., Ste. 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA

ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/983,502  
FILING DATE: 16-JAN-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/10521  
FILING DATE: 14-JUN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 114,615  
FILING DATE: 16-JUL-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 114,986  
FILING DATE: 17-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 115,319  
FILING DATE: 14-SEP-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 116,588  
FILING DATE: 27-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 117,932  
FILING DATE: 16-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Browdy, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: WALLACH-19  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-5197  
TELEFAX: (202) 737-3528  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 277 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-983-502-30

Query Match 44.5%; Score 718; DB 4; Length 277;  
Best Local Similarity 50.5%; Pred. No. 3.5e-73;  
Matches 143; Conservative 51; Mismatches 77; Indels 12; Gaps 3;

QY 19 EDSVDKPRDSSVPSLFSKSKKKVNTKRTDRVPTVQYNNFELGKCIINKNF 78  
Db 5 ENSVDSKIR-NLEPKIIHGESMDSGISLDNS-----YKMDYPEMGICIIINKNF 55  
QY 79 DKYTGKGVNRGTGDAEALFKCFRSLGFDYIVYNDSCAKMODILKKAASEDHNAACFA 138  
Db 56 HKSTGMSRSGTDVDANLRETFRNKLYEVNKNNDLREIVELMRVSKEDHSKRSSFV 115  
QY 139 CILLSHGEENVYIGKDVPTPIKDLTAHFRGDRCKTLLEKPKLFIOACRGTELDLDAIOAD 198  
Db 116 CULLSHGEEGIIFGTNGPVLKKTITNFRGDRCSLTGKPKLFIIOACRGTELDGCIETD 175  
QY 199 SGPINDTDANPRKPIPEADFLFAFSTVPGYYSRSPGSGMFVQALCSILEHCKELEI 258  
Db 176 SGVDDMAC--HKIPVADDFLVAYSTAPGYYSRNSKDSGFWFQSLCAMLKQYADKLEF 232  
QY 259 MQLITRVNDRVARHFESQSDPHHEKKQIPCVVSMLTKELYF 301  
Db 233 MHLITRVNKRKVAEFESFSDATFPAKQIPCIIVSMLTKELYF 275

RESULT 13  
PCT-US96-10521-30  
Sequence 30, Application PC/TUS9610521  
GENERAL INFORMATION:  
APPLICANT:

```

; GENERAL INFORMATION:
; APPLICANT: Alnemil, Emaad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
; FILE REFERENCE: 480140.431D2
; CURRENT APPLICATION NUMBER: US/09/954,697
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-954-697-27

Query Match      26.1%; Score 420.5; DB 10; Length 476;
Best Local Similarity 37.4%; Pred. No. 4.4e-35;
Matches 98; Conservative 43; Mismatches 90; Indels 31; Gaps 7;

QY 60 YNNMFEKLGKCIILNNKRF-----DKVTGMGVNNGTDKDAEALFKCFRSLGFDVYIN 112
    | : : : | | | | | | : : : | | | | | | : : : |
Db 223 YOMSKSPRGYCLILNNHFAKAREKVPRLHSIRONGTHLDAGALTTFEELHFEIKDHH 282

QY 113 DCSGAKMODLLKRSBEDHTNACFACILSHGEENVYIGKD-VTPIKDLTAHFRGDR 171
    | : : : | | | | | | : : : | | | | | | : : : |
Db 283 DCTVEQIYEILKITYQLMDHSMADCFICILSHGDKGIYTGDEAPLYELTSOFTGLKC 342

QY 172 KTLLEKRLFEFIOACRGTELDALIQADSGPINDTDANP-----RKIKIPEADFL 220
    | : : : | | | | | | : : : | | | | | | : : : |
Db 343 PSLGKRKRFVFIQACGDNVQKGIPIVET---DSEQPYLEMDLSSPQTRV-IPEDAFLL 397

QY 221 FAYSTVGYIYMRSPGRGSMFVQALCSLLEH-GKELEIMQILTRVNDVRAHFESQSD 279
    | : : : | | | | | | : : : | | | | | | : : : |
Db 398 LGMATVNNCVSYRNPACTWYIOSLCOSLRERCPRGDILITLLEVN-----YEVSKMD 451

QY 280 PHFEKKOIPCVCVSMITKELF 301
    | : : : | | | | | | : : : |
Db 452 DKMMGKOMPOTFTLRKKLVF 473

RESULT 15
US-09-962-834A-2
; Sequence 2, Application US/09962834A
; Patent No. US20020034813A1
; GENERAL INFORMATION:
; APPLICANT: Bowman, Michael
; TITLE OF INVENTION: NOVEL PROTEASE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; City: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/962,834A
; FILING DATE: 25-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/675,123
; FILING DATE: 1996-07-03
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15276
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224

```

```

; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 521 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-962-834A-2

Query Match      24.5%; Score 395; DB 10; Length 521;
Best Local Similarity 30.4%; Pred. No. 2e-32;
Matches 95; Conservative 55; Mismatches 99; Indels 64; Gaps 9;

QY 11 QGVEDSANEDSV-----DAKPDRS-----SEVPSLFSSKKKNVTRSI--KT 50
    | : : : | | | | | | : : : | | | | | | : : : |
Db 209 QGEELVSGTDVKTFLFLEALPQESQWKNHAGSNGNRATNGAPSLVSHGMOGASANTINSET 268

QY 51 TDRVPTIYNNMFEKLGKCIILNNKRPDKVYGMVNRNGTDKDAEALFKCFRSLGFDVY 110
    | : : : | | | | | | : : : | | | | | | : : : |
Db 269 STKRAVYVRMNNRHR--GLCVIVNHSF--TSLKDRGTHKDAEILSHVFWLGFVTHI 323

QY 111 YNDCGAKMODLLKRS--BEDHTNACFACILSHGEENVYIGKD-GVTPIKDLTAHFRG 168
    | : : : | | | | | | : : : | | | | | | : : : |
Db 324 HNNVTKEEMVYLOKQKCNPAHADGDCVFICILTHGERFGAVISSDALIPRILMSHFT 383

QY 169 DRCKTLEKPKLFIOACRGTELDALIQADSGPINDTD--NPRYKIPVADFLFAYSTV 226
    | : : : | | | | | | : : : | | | | | | : : : |
Db 384 LQCPRLAEKPKLFIOACGGEIOPSVSLEADALNEQAPTSIQDSIPRPAEDLGLATV 443

QY 227 PGYIYMRSPGRGSMFVQALCSLLEH-GKELEIMQILTRVNDVRAHFESQSDPHHEK 286
    | : : : | | | | | | : : : | | | | | | : : : |
Db 444 PGYVGFHRYHEEGSWYIOSLCN-----HLKK 468

QY 287 QIPCVSMITKEL 299
    | : : : | | | | | | : : : |
Db 469 LVPRMLKLEKTM 481

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Search completed: December 2, 2002, 13:04:18  
 Job time : 9.35862 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 2, 2002, 12:54:49 ; Search time 14.1052 Seconds  
(Without alignments)  
632.048 Million cell updates/sec

Title: US-09-895-263-2

Perfect score: 1613

Sequence: 1 MADDCGICEPQGVDSANED.....EKKQIPCVSMILKELVFSQ 303

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/6CTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1613	100.0	303	US-08-462-969B-2	Sequence 2, Appl
2	1606	99.6	303	US-09-561-756-24	Sequence 24, Appl
3	1606	99.6	303	US-09-227-721-24	Sequence 24, Appl
4	1606	99.6	303	US-08-556-627A-2	Sequence 2, Appl
5	721	44.7	277	US-08-591-605-2	Sequence 2, Appl
6	721	44.7	277	US-08-964-308-6	Sequence 6, Appl
7	721	44.7	277	US-08-462-969B-4	Sequence 6, Appl
8	721	44.7	277	US-08-964-313-6	Sequence 6, Appl
9	721	44.7	277	US-09-069-138-6	Sequence 6, Appl
10	718	44.5	277	US-09-561-756-12	Sequence 12, Appl
11	718	44.5	277	US-09-227-721-12	Sequence 12, Appl
12	718	44.5	277	US-08-983-502-30	Sequence 30, Appl
13	718	44.5	277	PCR-US96-10521-30	Sequence 30, Appl
14	711	44.1	277	US-08-964-308-10	Sequence 10, Appl
15	711	44.1	277	US-08-964-313-10	Sequence 10, Appl
16	711	44.1	277	US-09-069-138-10	Sequence 10, Appl
17	709	44.0	277	US-08-890-542A-2	Sequence 2, Appl
18	552	34.2	299	US-08-773-608A-2	Sequence 2, Appl
19	474	29.4	293	US-09-561-756-21	Sequence 21, Appl
20	474	29.4	293	US-09-227-721-21	Sequence 21, Appl
21	468	29.0	278	US-08-522-813-4	Sequence 21, Appl
22	466	28.9	293	US-08-446-923-5	Sequence 5, Appl
23	466	28.9	293	US-09-146-331-5	Sequence 5, Appl
24	466	28.9	293	US-08-896-885-5	Sequence 5, Appl
25	466	28.9	293	US-09-375-256-5	Sequence 5, Appl
26	466	28.9	293	US-08-983-502-31	Sequence 31, Appl
27	466	28.9	293	US-09-376-156-5	Sequence 5, Appl

28	466	28.9	293	5	PCT-US96-10521-31	Sequence 31, Appl
29	444.5	27.6	346	2	US-08-618-408B-2	Sequence 2, Appl
30	444.5	27.6	479	1	US-08-665-220-2	Sequence 2, Appl
31	444.5	27.6	479	4	US-09-291-692-2	Sequence 2, Appl
32	444.5	27.6	479	4	US-09-561-756-33	Sequence 33, Appl
33	444.5	27.6	479	4	US-09-227-721-33	Sequence 27, Appl
34	426.5	26.4	479	4	US-08-382-155-27	Sequence 27, Appl
35	425.5	26.4	479	4	US-08-983-502-7	Sequence 12, Appl
36	425.5	26.4	479	5	PCT-US96-10521-7	Sequence 7, Appl
37	424.5	26.3	479	4	US-08-807-200-12	Sequence 26, Appl
38	424.5	26.3	479	4	US-09-382-155-26	Sequence 26, Appl
39	424.5	26.3	479	4	US-09-382-155-28	Sequence 28, Appl
40	424.5	26.3	479	4	US-09-001-777-12	Sequence 12, Appl
41	424.5	26.3	479	4	US-09-074-044A-26	Sequence 26, Appl
42	424.5	26.3	479	4	US-09-074-044A-27	Sequence 27, Appl
43	424.5	26.3	479	4	US-09-074-044A-28	Sequence 28, Appl
44	423.5	26.3	286	4	US-09-360-017-1	Sequence 1, Appl
45	423.5	26.3	389	2	US-08-618-408B-4	Sequence 4, Appl

#### ALIGNMENTS

RESULT 1  
US-08-462-969B-2  
Sequence 2, Application US/08462969B  
Patent No. 6087150  
GENERAL INFORMATION:  
APPLICANT: He, Wei-Wu et al.  
TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme  
TITLE OF INVENTION: Like Apoptosis Protease 3 and 4  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Ave.  
CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/462,969B  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/334,251  
FILING DATE: 11-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Brookes, A. Anders  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PF140P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8439  
INFORMATION FOR SEQ. ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 303 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-462-969B-2  
Query Match 100.0%; Score 1613; DB 3; Length 303;  
Best local Similarity 100.0%; Pred. No. 1e-174;  
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 MADDCGICEPQGVDSANEDVDKPRSSFPVLSKRRKNTMRSIKTRDVPYQY 60  
|||||

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Db 1 MADDGCIIEGVEDSANDSVDAKPDSSFPVPSLFSSKKKNVTMRSIKTTDRVPPTYOY 60
QY 61 NNNFEKLGKCIITNNKNFDPKVTGMGVRNGTDDAEALFCFSLGSDVYVYNDCCSAKMQ 120
Db 61 NNNFEKLGKCIITNNKNFDPKVTGMGVRNGTDDAEALFCFSLGSDVYVYNDCCSAKMQ 120
QY 121 DLKKAASEDHNTNACFACILSHGSEENVYIGKDGVTPIKDLTAHFRGRCRCTLLEKPKL 180
Db 121 DLKKAASEDHNTNACFACILSHGSEENVYIGKDGVTPIKDLTAHFRGRCRCTLLEKPKL 180
QY 121 DLKKAASEDHNTNACFACILSHGSEENVYIGKDGVTPIKDLTAHFRGRCRCTLLEKPKL 180
Db 121 DLKKAASEDHNTNACFACILSHGSEENVYIGKDGVTPIKDLTAHFRGRCRCTLLEKPKL 180
QY 181 FFIOACRGTLEDLDAIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSM 240
Db 181 FFIOACRGTLEDLDAIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSM 240
QY 241 FVOALCSILIEHGKLEIMQILTRVNDVRAHRESQSDDPHHEKQKQIPCVVSMLTKELY 300
Db 241 FVOALCSILIEHGKLEIMQILTRVNDVRAHRESQSDDPHHEKQKQIPCVVSMLTKELY 300
QY 301 FSO 303
Db 301 FSO 303
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```
RESULT 2
US-09-561-756-24 ; Sequence 24, Application US/09561756
; Patent No. 6376226
; GENERAL INFORMATION:
; APPLICANT: Alnemrl, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 480140.431
; CURRENT APPLICATION NUMBER: US/09/561.756
; CURRENT FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 09/227,721
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-561-756-24
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Query Match 99.6%; Score 1606; DB 4; Length 303;
Best Local Similarity 99.3%; Pred. No. 6.4e-174;
Matches 301; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 1 MADDGCIIEGVEDSANDSVDAKPDSSFPVPSLFSSKKKNVTMRSIKTTDRVPPTYOY 60
Db 1 MADDGCIIEGVEDSANDSVDAKPDSSFPVPSLFSSKKKNVTMRSIKTTDRVPPTYOY 60
QY 61 NNNFEKLGKCIITNNKNFDPKVTGMGVRNGTDDAEALFCFSLGSDVYVYNDCCSAKMQ 120
Db 61 NNNFEKLGKCIITNNKNFDPKVTGMGVRNGTDDAEALFCFSLGSDVYVYNDCCSAKMQ 120
QY 121 DLKKAASEDHNTNACFACILSHGSEENVYIGKDGVTPIKDLTAHFRGRCRCTLLEKPKL 180
Db 121 DLKKAASEDHNTNACFACILSHGSEENVYIGKDGVTPIKDLTAHFRGRCRCTLLEKPKL 180
QY 121 DLKKAASEDHNTNACFACILSHGSEENVYIGKDGVTPIKDLTAHFRGRCRCTLLEKPKL 180
Db 121 DLKKAASEDHNTNACFACILSHGSEENVYIGKDGVTPIKDLTAHFRGRCRCTLLEKPKL 180
QY 181 FFIOACRGTLEDLDAIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSM 240
Db 181 FFIOACRGTLEDLDAIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSM 240
QY 241 FVOALCSILIEHGKLEIMQILTRVNDVRAHRESQSDDPHHEKQKQIPCVVSMLTKELY 300
Db 241 FVOALCSILIEHGKLEIMQILTRVNDVRAHRESQSDDPHHEKQKQIPCVVSMLTKELY 300
QY 301 FSO 303
Db 301 FSO 303
```

```
RESULT 3
US-09-227-721-24 ; Sequence 24, Application US/09227721
; Patent No. 6379950
; GENERAL INFORMATION:
; APPLICANT: Alnemrl, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 480140.431
; CURRENT APPLICATION NUMBER: US/09/227,721
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-227-721-24
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```
Query Match 99.6%; Score 1606; DB 4; Length 303;
Best Local Similarity 99.3%; Pred. No. 6.4e-174;
Matches 301; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 1 MADDGCIIEGVEDSANDSVDAKPDSSFPVPSLFSSKKKNVTMRSIKTTDRVPPTYOY 60
Db 1 MADDGCIIEGVEDSANDSVDAKPDSSFPVPSLFSSKKKNVTMRSIKTTDRVPPTYOY 60
QY 61 NNNFEKLGKCIITNNKNFDPKVTGMGVRNGTDDAEALFCFSLGSDVYVYNDCCSAKMQ 120
Db 61 NNNFEKLGKCIITNNKNFDPKVTGMGVRNGTDDAEALFCFSLGSDVYVYNDCCSAKMQ 120
QY 121 DLKKAASEDHNTNACFACILSHGSEENVYIGKDGVTPIKDLTAHFRGRCRCTLLEKPKL 180
Db 121 DLKKAASEDHNTNACFACILSHGSEENVYIGKDGVTPIKDLTAHFRGRCRCTLLEKPKL 180
QY 181 FFIOACRGTLEDLDAIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSM 240
Db 181 FFIOACRGTLEDLDAIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSM 240
QY 241 FVOALCSILIEHGKLEIMQILTRVNDVRAHRESQSDDPHHEKQKQIPCVVSMLTKELY 300
Db 241 FVOALCSILIEHGKLEIMQILTRVNDVRAHRESQSDDPHHEKQKQIPCVVSMLTKELY 300
QY 301 FSO 303
Db 301 FSO 303
```

```
RESULT 4
US-08-556-627A-2 ; Sequence 2, Application US/08556627A
; Patent No. 6462175
; GENERAL INFORMATION:
; APPLICANT: Alnemrl, Emad S.
; APPLICANT: Fernandes-Alnemrl, Teresa
; APPLICANT: Litwack, Gerald
; APPLICANT: Armstrong, Robert
; APPLICANT: Tomaselli, Kevin
; TITLE OF INVENTION: Mch3, A No. 6462175el Apoptotic Protease,
; TITLE OF INVENTION: Nucleic Acids Encoding and Methods of Use
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
```

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/556,627A  
FILING DATE: 13-NOV-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-ID 1813  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 303 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-556-627A-2

Query Match 99.6%; Score 1606; DB 4; Length 303;  
Best Local Similarity 99.3%; Pred. No. 6.4e-174;

Matches 301; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MADDGCIIEGVEDSANDSDYDAKDRSSFPVSLFSKKKNTMRSIKTRDRVPPTYQY 60  
DB 1 MADDGCIIEGVEDSANDSDYDAKDRSSFPVSLFSKKKNTMRSIKTRDRVPPTYQY 60  
QY 61 MNFELGICIIINNNKFNKVTGMGRNGTDKAEALFCFRSLGSDVIYNNCSACKM 120  
DB 61 MNFELGICIIINNNKFNKVTGMGRNGTDKAEALFCFRSLGSDVIYNNCSACKM 120  
QY 121 DLLKASEEDHTNAFCACILSHGSEENVYKDGVTPIKDLTAHFRGDRCKTLLEKPKL 180  
DB 121 DLLKASEEDHTNAFCACILSHGSEENVYKDGVTPIKDLTAHFRGDRCKTLLEKPKL 180  
QY 181 FFIQACRGTELDIAOASGPINDTDANPRKIPVEADFLFAVSTVPGYYSWSPGSGW 240  
DB 181 FFIQACRGTELDIAOASGPINDTDANPRKIPVEADFLFAVSTVPGYYSWSPGSGW 240  
QY 241 FVOALCSIIIEHGEKELEIMQILTRVNDVRAHRESOSDDPHHEKKOICVSMLTRELY 300  
DB 241 FVOALCSIIIEHGEKELEIMQILTRVNDVRAHRESOSDDPHHEKKOICVSMLTRELY 300  
QY 301 FSQ 303  
DB 301 FSQ 303

## RESULT 5

US-08-591-605-2  
Sequence 2, Application US/08591605  
Patent No. 6060238  
GENERAL INFORMATION:  
APPLICANT: Dixit, Vishva M.  
TITLE OF INVENTION: METHOD AND COMPOSITION FOR REGULATING  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/591,605  
FILING DATE: 09-FEB-1996  
CLASSIFICATION: 514

## ATTORNEY/AGENT INFORMATION:

NAME: KOSKI, ANTOINETTE F.  
REGISTRATION NUMBER: 34,202  
REFERENCE/DOCKET NUMBER: 20344-21036.21  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141 MRSNFOERS SFO  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 277 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-591-605-2

Query Match 44.7%; Score 721; DB 3; Length 277;  
Best Local Similarity 50.9%; Pred. No. 1.6e-73;

Matches 144; Conservative 50; Mismatches 77; Indels 12; Gaps 3;

QY 19 EDGVDKPDSSFPVSLFSKKKNTMRSIKTRDRVPPTYQYNNMFKLGKCIINNNKF 78  
DB 5 ENSVDSKSIK-NLEPKTIHGESMDGSLDNS-----YKMDYDEMGLCIIINNNKF 55  
QY 79 DKVTGMGRNGTDKAEALFCFRSLGSDVIYNNCSACKMDDLKASEEDHTNAFCFA 138  
DB 56 HKSTGMTSRSGTVDANLANLRETNKLYEVKNKNDLREELVELMRVSEDSKRSSEV 115  
QY 139 CILSHGSEENVYKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQAACRGTELDIAO 198  
DB 116 CVLSHGSEENVYKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQAACRGTELDIAO 175  
QY 199 SCPIINDTANPRKIPVEADFLFAVSTVPGYYSWSPGSGWFOALCSIIIEHGEKELEI 258  
DB 176 SGVDDDMAC---HKIPVEADFLFAVSTVPGYYSWSPGSGWFOALCSIIIEHGEKELEI 232  
QY 259 MQLTRVNDVRAHRESOSDDPHHEKKOICVSMLTRELY 301  
DB 233 MQLTRVNDVRAHRESOSDDPHHEKKOICVSMLTRELY 275

## RESULT 6

US-08-964-308-6  
Sequence 6, Application US/08964308  
Patent No. 6066715  
GENERAL INFORMATION:  
APPLICANT: DESMARAIS, SYLVIE  
APPLICANT: FRIESEN, RICHARD  
APPLICANT: ZAMBONI, ROBERT  
TITLE OF INVENTION: NEW LIGANDS FOR PHOSPHATASE  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ROBERT J. NORTH - MERCK & CO., INC.  
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000  
CITY: RAHWAY  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Diskette  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/964,308  
FILING DATE: 04-NOV-1996  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: NORTH, ROBERT J.  
REGISTRATION NUMBER: 27,366  
REFERENCE/DOCKET NUMBER: 19840 PCT  
TELECOMMUNICATION INFORMATION:







Db 116 CULLSHGEEGIIIFCTNGPVDIKITTFRRGDRCSLNGPKLFIIOACRGTELDGIEFD 175  
QY 199 SGPINDTANPRKIPYEADELFAVSTVPGYYSWRSPGSGWFOALCSIIIEHKELEI 258  
Db 176 SGVDDMAC--HKIPVADFLVAYSTAPGYYSWRNSKDGSMFIOSLCAMLKOYADKLEF 232  
QY 259 MQLITRVNDRVARHFEOSODPHHEKKQIPCVYSMLTKELYF 301  
Db 233 MHLITRVNKRVAIEFESEFSDATFHAKKQIPCIYSMLTKELYF 275

## RESULT 11

US-09-227-721-12  
; Sequence 12, Application US/09227721  
; Patent No. 6379950  
; GENERAL INFORMATION:  
; APPLICANT: Alnemt, Emad S.  
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES  
; FILE REFERENCE: 480140.431  
; CURRENT APPLICATION NUMBER: US/09/227,721  
; CURRENT FILING DATE: 1999-01-08  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 12  
; LENGTH: 277  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-227-721-12

Query Match 44.5%; Score 718; DB 4; Length 277;  
Best Local Similarity 50.5%; Pred. No. 3.5e-73;

Matches 143; Conservative 51; Mismatches 77; Indels 12; Gaps 3;

QY 19 EDSVDAPDRSSFPVPSLFSSKKKNVTMRISITKTRDVPYTYOYNNFEKLCIITNNKNF 78  
Db 5 ENSVDSKSIK-NLEPKIIHGESMSDGSISLDSN-----YKNDYEMGICIIITNNKNF 55  
QY 79 DKYTGKVRNGTGDADALFKCFPSLGFVIVYNDSCAKMODLLKASEDHTNAACFA 138  
Db 56 HKSTGMTSRSGTVDANLKRTPFNKLYEVNKNNDLREELVELMRVSKEDHSKRSSFV 115  
QY 139 CILLSHGEENVYIGKDVTPIKDLTAHFRGDRCKTLEKPLFIIOACRGTELDADIAOD 198  
Db 116 CULLSHGEEGIIIFCTNGPVDIKITTFRRGDRCSLNGPKLFIIOACRGTELDGIEFD 175  
QY 199 SGPINDTANPRKIPYEADELFAVSTVPGYYSWRSPGSGWFOALCSIIIEHKELEI 258  
Db 176 SGVDDMAC--HKIPVADFLVAYSTAPGYYSWRNSKDGSMFIOSLCAMLKOYADKLEF 232  
QY 259 MQLITRVNDRVARHFEOSODPHHEKKQIPCVYSMLTKELYF 301  
Db 233 MHLITRVNKRVAIEFESEFSDATFHAKKQIPCIYSMLTKELYF 275

## RESULT 12

US-08-983-502-30  
; Sequence 30, Application US/08983502  
; Patent No. 6399327  
; GENERAL INFORMATION:  
; APPLICANT: David WALLACH  
; APPLICANT: Mark P. BOLDIN  
; APPLICANT: Tanya M. GONCHAROV  
; APPLICANT: Yury V. GOLTSEV  
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS  
; TITLE OF INVENTION: AND OTHER PROTEINS  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Browdy and Neimark  
; STREET: 419 Seventh Street N.W., Ste. 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA

ZIP: 20004  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/983,502  
FILING DATE: 16-JAN-1998

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/10521  
FILING DATE: 14-JUN-1996

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 114,615  
FILING DATE: 16-JUL-1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 114,986  
FILING DATE: 17-AUG-1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 115,319  
FILING DATE: 14-SEP-1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 116,588  
FILING DATE: 27-DEC-1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 117,932  
FILING DATE: 16-APR-1996

ATTORNEY/AGENT INFORMATION:  
NAME: Browdy, Roger L.  
REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: WALLACH-19  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-5197  
TELEFAX: (202) 737-3528

INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:

LENGTH: 277 amino acids  
TYPE: amino acid

STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: protein  
US-08-983-502-30

Query Match 44.5%; Score 718; DB 4; Length 277;  
Best Local Similarity 50.5%; Pred. No. 3.5e-73;

Matches 143; Conservative 51; Mismatches 77; Indels 12; Gaps 3;

QY 19 EDSVDAPDRSSFPVPSLFSSKKKNVTMRISITKTRDVPYTYOYNNFEKLCIITNNKNF 78  
Db 5 ENSVDSKSIK-NLEPKIIHGESMSDGSISLDSN-----YKNDYEMGICIIITNNKNF 55  
QY 79 DKYTGKVRNGTGDADALFKCFPSLGFVIVYNDSCAKMODLLKASEDHTNAACFA 138  
Db 56 HKSTGMTSRSGTVDANLKRTPFNKLYEVNKNNDLREELVELMRVSKEDHSKRSSFV 115  
QY 139 CILLSHGEENVYIGKDVTPIKDLTAHFRGDRCKTLEKPLFIIOACRGTELDADIAOD 198  
Db 116 CULLSHGEEGIIIFCTNGPVDIKITTFRRGDRCSLNGPKLFIIOACRGTELDGIEFD 175  
QY 199 SGPINDTANPRKIPYEADELFAVSTVPGYYSWRSPGSGWFOALCSIIIEHKELEI 258  
Db 176 SGVDDMAC--HKIPVADFLVAYSTAPGYYSWRNSKDGSMFIOSLCAMLKOYADKLEF 232  
QY 259 MQLITRVNDRVARHFEOSODPHHEKKQIPCVYSMLTKELYF 301  
Db 233 MHLITRVNKRVAIEFESEFSDATFHAKKQIPCIYSMLTKELYF 275

## RESULT 13

PCT-US96-10521-30  
; Sequence 30, Application PC/TUS9610521  
; GENERAL INFORMATION:  
; APPLICANT:

```

; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
; TITLE OF INVENTION: AND OTHER PROTEINS
; NUMBER OF SEQUENCES: 34
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10521
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 114,615
; FILING DATE: 16-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 114,986
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 115,319
; FILING DATE: 14-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 116,588
; FILING DATE: 27-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 117,932
; FILING DATE: 16-APR-1996
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-10521-30

Query Match 44.5%; Score 718; DB 5; Length 277;
Best Local Similarity 50.5%; Pred. No. 3.5e-73;
Matches 143; Conservative 51; Mismatches 77; Indels 12; Gaps 3;

QY 19 EDSVAKPDRSSVPSLSKSKKNTMRISIKTRDRVPTVYQYNNFEKLGKCIINKNF 78
DB 5 ENSVDKSKIK-NLEPKIIHSGESMDGSLDMS-----YKMDYPEMGLCIIINKNF 55

QY 79 DKVTAGVNRGTDKDAEALFKCFRSLGFYIYVNDSCAMODLLKASEEDHTNAACRA 138
DB 56 HKSTGTSRSGTDVDANLRETFRNLYEVNRKNDLTREIIVELMDVSKEDSKRSSFV 115

QY 139 CILSHGEENVYIGKDGVPYIKDLTAHFGRDCKTLEKPKLFFIOACRGTELDADIAOD 198
DB 116 CYLLSHGEGGIIIFGTNGPYDLAKITNEFRGDKRSLTGKPKLFIIOACRGTELDGCIETD 175

QY 199 SCPIINDTANPRKRIPEADFLPAYSTGVYYSWRSPGRSGSWFOALCSILEHGELEI 258
DB 176 SGVDDDMAC--HKIPVADFLPAYSTAGYYSWRNSKDSWFIQSICAMLKQYADKLEF 232

QY 259 MQLTRVNDVARHFEQSDDPHFEKKOIPCVVSMLTKELYF 301
DB 233 MHLTRVNRKVAEFESFSDATFAKKOIPCIYVSMLTKELYF 275

RESULT 14
US-08-964-308-10
; Sequence 10, Application US/08964308
; Patent No. 6066715
; GENERAL INFORMATION:
; APPLICANT: DESMARAIS, SYLVIE
; APPLICANT: FRIESEN, RICHARD
; APPLICANT: ZAMRONI, ROBERT
; TITLE OF INVENTION: NEW LIGANDS FOR PHOSPHATASE
; TITLE OF INVENTION: BINDING ASSAY
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: ROBERT J. NORTH - MERCK & CO., INC.
; STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/964,308
; FILING DATE: 04-NOV-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: NORTH, ROBERT J
; REGISTRATION NUMBER: 27,366
; REFERENCE/DOCKET NUMBER: 19840 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-7262
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-964-308-10

Query Match 44.1%; Score 711; DB 3; Length 277;
Best Local Similarity 50.5%; Pred. No. 2.2e-72;
Matches 143; Conservative 50; Mismatches 78; Indels 12; Gaps 3;

QY 19 EDSVAKPDRSSVPSLSKSKKNTMRISIKTRDRVPTVYQYNNFEKLGKCIINKNF 78
DB 5 ENSVDKSKIK-NLEPKIIHSGESMDGSLDMS-----YKMDYPEMGLCIIINKNF 55

QY 79 DKVTAGVNRGTDKDAEALFKCFRSLGFYIYVNDSCAMODLLKASEEDHTNAACRA 138
DB 56 HKSTGTSRSGTDVDANLRETFRNLYEVNRKNDLTREIIVELMDVSKEDSKRSSFV 115

QY 139 CILSHGEENVYIGKDGVPYIKDLTAHFGRDCKTLEKPKLFFIOACRGTELDADIAOD 198
DB 116 CYLLSHGEGGIIIFGTNGPYDLAKITNEFRGDKRSLTGKPKLFIIOACRGTELDGCIETD 175

QY 199 SCPIINDTANPRKRIPEADFLPAYSTGVYYSWRSPGRSGSWFOALCSILEHGELEI 258
DB 176 SGVDDDMAC--HKIPVADFLPAYSTAGYYSWRNSKDSWFIQSICAMLKQYADKLEF 232

QY 259 MQLTRVNDVARHFEQSDDPHFEKKOIPCVVSMLTKELYF 301
DB 233 MHLTRVNRKVAEFESFSDATFAKKOIPCIYVSMLTKELYF 275

RESULT 15
US-08-964-313-10
; Sequence 10, Application US/08964313
; Patent No. 6114132
; GENERAL INFORMATION:
; APPLICANT: DESMARAIS, SYLVIE
; APPLICANT: FRIESEN, RICHARD
; APPLICANT: GRESSER, MICHAEL
; APPLICANT: KENNEDY, BRIAN
; APPLICANT: NICHOLSON, DONALD
; APPLICANT: RAMACHANDRAN, CHITDAMBARAN
; APPLICANT: SKOREY, KATHRYN
; APPLICANT: FORD-HUTCHINSON, ANTHONY
; TITLE OF INVENTION: PHOSPHATASE BINDING ASSAY
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:

```

ADDRESSEE: PHILIPPE L. DURETTE - MERCK & CO., INC.  
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000  
CITY: RAHWAY  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/964,313  
FILING DATE: 04-NOV-1997  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/030,408  
FILING DATE: 04-NOV-1996  
APPLICATION NUMBER: PCT/CA97/00825

FILING DATE: 03-NOV-1996  
ATTORNEY/AGENT INFORMATION:

NAME: DURETTE, PHILIPPE L.  
REGISTRATION NUMBER: 35,125

REFERENCE/DOCKET NUMBER: 19824Y  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 732-594-4568  
TELEFAX: 732-594-4720  
TELEX:

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 277 amino acids  
TYPE: amino acid

STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: peptide  
US-08-964-313-10

Query Match 44.1%; Score 711; DB 3; Length 277;  
Best Local Similarity 50.5%; Pred. No. 2, 2e-72;

Matches 143; Conservative 50; Mismatches 78; Indels 12; Gaps 3;

QY 19 EDSVDAKPDSSFPVPSLFSKRRKNTMRISIKTTRDVRVPTVYQNMNFEKLGKIIINKNF 78  
DB 5 ENSYDSKSIK-NLEPKIHGSESMDSGLDNS-----YKMDYPMGCLIIINKNF 55  
QY 79 DVTGNGVANGTDKDAEALFKCFRSLGFVYIYNDSCAKMODLLKASEEDHTNACFA 138  
DB 56 HKSTGTSRSRGTVDVAANLRETFRNKLYEVRNKNDLTREIYELMRDVSKEHRSKRSFV 115  
QY 139 CILSHGEENVYIGKGVPIKDLTAHFRGDRCKTILEKPKLFYIOACRSTELDAIQA 198  
DB 116 CVLLSHGEGCIIIFGNGPVLKKTINFERGDRSLTGKPKLFIIOASRGTELDCGIEFD 175  
QY 199 SGPINDTDANPRKILPEADFLFAYSTVPGYYSWRSPGRGSMFVQALCSILEHSGKELEI 258  
DB 176 SGVDDDMAC---HKIPVEADFLFAYSTAGYYSWRNSKSGSMFIOSLCAMLKQYADKLEF 232  
QY 259 MOILTRVNDVRAHRESOSDDPHFEKKQIPCVSMLTRKELYE 301  
DB 233 MHLTRVNRKVALEFESFSDATFPAKKQIPCIIVSMLTRKELYE 275

Search completed: December 2, 2002, 12:58:44  
Job time: 16.1052 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 2, 2002, 12:54:49 ; Search time 12.8948 Seconds  
(without alignments)  
632.048 Million cell updates/sec

Title: US-09-895-263-4

Perfect score: 1463

Sequence: 1 MENTENSVDKSKIKNLEPKI.....AKKQIPCIYSMLTKELFYH 277

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 segs, 2942222 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents-AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/6C.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/6D.COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1463	100.0	277	3	US-08-591-605-2
2	1463	100.0	277	3	US-08-964-308-6
3	1463	100.0	277	3	US-08-462-969B-4
4	1463	100.0	277	3	US-08-964-313-6
5	1463	100.0	277	4	US-09-069-138-6
6	1460	99.8	277	4	US-09-561-756-12
7	1460	99.8	277	4	US-09-227-721-12
8	1460	99.8	277	4	US-08-983-502-30
9	1460	99.8	277	5	PCT-US96-10521-30
10	1453	99.3	277	3	US-08-964-308-10
11	1453	99.3	277	3	US-08-964-313-10
12	1453	99.3	277	4	US-09-069-138-10
13	1304	89.1	277	2	US-08-890-542A-2
14	912	62.3	290	4	US-09-561-756-34
15	912	62.3	290	4	US-09-227-721-34
16	896	61.2	285	4	US-09-561-756-35
17	896	61.2	285	4	US-09-561-756-35
18	761	52.0	148	3	US-08-964-308-11
19	761	52.0	148	4	US-08-964-313-11
20	761	52.0	148	4	US-09-069-138-11
21	725	49.6	303	4	US-09-561-756-24
22	725	49.6	303	4	US-09-227-721-24
23	725	49.6	303	4	US-08-556-627A-2
24	721	49.3	293	4	US-08-462-969B-2
25	525.5	35.9	293	4	US-09-561-756-21
26	525.5	35.9	293	4	US-09-227-721-21
27	517.5	35.4	293	1	US-08-446-925-5

28	517.5	35.4	293	2	US-09-146-331-5	Sequence 5, Appl
29	517.5	35.4	293	2	US-08-896-885-5	Sequence 5, Appl
30	517.5	35.4	293	4	US-09-375-256-5	Sequence 5, Appl
31	517.5	35.4	293	4	US-08-983-502-31	Sequence 31, Appl
32	517.5	35.4	293	4	US-09-376-156-5	Sequence 5, Appl
33	517.5	35.4	293	5	PCT-US96-10521-31	Sequence 31, Appl
34	516.5	35.3	278	3	US-08-522-813-4	Sequence 4, Appl
35	470	32.1	299	2	US-08-773-608A-2	Sequence 4, Appl
36	429	29.3	476	4	US-09-561-756-27	Sequence 27, Appl
37	429	29.3	476	4	US-09-227-721-27	Sequence 27, Appl
38	423	28.9	286	4	US-09-360-017-1	Sequence 1, Appl
39	421	28.8	389	2	US-08-618-408B-4	Sequence 4, Appl
40	421	28.8	464	4	US-08-983-502-18	Sequence 18, Appl
41	421	28.8	464	5	PCT-US96-10521-18	Sequence 18, Appl
42	421	28.8	479	4	US-08-983-502-7	Sequence 7, Appl
43	421	28.8	479	5	PCT-US96-10521-7	Sequence 7, Appl
44	421	28.8	496	1	US-08-665-220-4	Sequence 4, Appl
45	421	28.8	496	4	US-09-291-692-4	Sequence 4, Appl

#### ALIGNMENTS

RESULT 1  
US-08-591-605-2  
Sequence 2, Application US/08591605  
Patent No. 6060238  
GENERAL INFORMATION:  
APPLICANT: Dixit, Vishva M.  
TITLE OF INVENTION: METHOD AND COMPOSITION FOR REGULATING  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/591,605  
FILING DATE: 09-FEB-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: KOSKI, ANTOINETTE F.  
REGISTRATION NUMBER: 34,202  
REFERENCE/DOCKET NUMBER: 20344-21036.21  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141 MRSNFOERS SFO  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 277 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-591-605-2

Query Match 100.0%; Score 1463; DB 3; Length 277;  
Best local Similarity 100.0%; Pred. No. 1.7e-161;  
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENTENSVDKSKIKNLEPKIHGSESDGSLDNGYKMDYPMGICITINNKRFHSTG 60  
|||||  
Db 1 MENTENSVDKSKIKNLEPKIHGSESDGSLDNGYKMDYPMGICITINNKRFHSTG 60  
QY 61 MRSRGTVDAAALRLRTFNLKYEVRNKNLDTREELVELMRDVSKEHDSKRSFVCLLS 120

Db 61 MTSSGTDVDANLRETFRNKLYEVNRKNDLTREIIVELMRDVSKEDESKSSFCVLLS 120  
QY 121 HGEGLIFGTNGPVDLKKITNFFRGDRCSLTGPKFLIIQACRGTELDGCIETDSGVD 180  
Db 121 HGEGLIFGTNGPVDLKKITNFFRGDRCSLTGPKFLIIQACRGTELDGCIETDSGVD 180  
QY 181 DMACHKIPVEADFLYASTAGYYSWRNSKDSGSMFIQSLCAMLKQYADKLEFMHILTRVN 240  
Db 181 DMACHKIPVEADFLYASTAGYYSWRNSKDSGSMFIQSLCAMLKQYADKLEFMHILTRVN 240  
QY 241 RKVATEFESFSDATFHAKKOIPCIYSMLTKELFYH 277  
Db 241 RKVATEFESFSDATFHAKKOIPCIYSMLTKELFYH 277

## RESULT 2

US-08-964-308-6  
; Sequence 6, Application US/08964308  
; Patent No. 6066715  
; GENERAL INFORMATION:  
; APPLICANT: DESMARAIS, SYLVIE  
; APPLICANT: FRIESEN, RICHARD  
; APPLICANT: ZAMBONI, ROBERT  
; TITLE OF INVENTION: NEW LIGANDS FOR PHOSPHATASE  
; TITLE OF INVENTION: BINDING ASSAY  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ROBERT J. NORTH - MERCK & CO., INC.  
; STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000  
; CITY: RAHWAY  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07065  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Diskette  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/964,308  
; FILING DATE: 04-NOV-1996  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: NORTH, ROBERT J  
; REGISTRATION NUMBER: 27,366  
; REFERENCE/DOCKET NUMBER: 19840 PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 732-594-7262  
; TELEFAX: 732-594-4720  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 277 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-964-308-6

Query Match 100.0%; Score 1463; DB 3; Length 277;  
Best Local Similarity 100.0%; Pred. No. 1,7e-161;  
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENTENSVDKSIKNLEPKIIHGSSEMDGSLDYSYKMDYEMGLCIIINKNFHKSTG 60  
Db 1 MENTENSVDKSIKNLEPKIIHGSSEMDGSLDYSYKMDYEMGLCIIINKNFHKSTG 60  
QY 61 MTSRSGTDVDANLRETFRNKLYEVNRKNDLTREIIVELMRDVSKEDESKSSFCVLLS 120  
Db 61 MTSRSGTDVDANLRETFRNKLYEVNRKNDLTREIIVELMRDVSKEDESKSSFCVLLS 120  
QY 121 HGEGLIFGTNGPVDLKKITNFFRGDRCSLTGPKFLIIQACRGTELDGCIETDSGVD 180  
Db 121 HGEGLIFGTNGPVDLKKITNFFRGDRCSLTGPKFLIIQACRGTELDGCIETDSGVD 180

Db 121 HGEGLIFGTNGPVDLKKITNFFRGDRCSLTGPKFLIIQACRGTELDGCIETDSGVD 180  
QY 181 DMACHKIPVEADFLYASTAGYYSWRNSKDSGSMFIQSLCAMLKQYADKLEFMHILTRVN 240  
Db 181 DMACHKIPVEADFLYASTAGYYSWRNSKDSGSMFIQSLCAMLKQYADKLEFMHILTRVN 240  
QY 241 RKVATEFESFSDATFHAKKOIPCIYSMLTKELFYH 277  
Db 241 RKVATEFESFSDATFHAKKOIPCIYSMLTKELFYH 277

## RESULT 3

US-08-462-969B-4  
; Sequence 4, Application US/08462969B  
; Patent No. 6087150  
; GENERAL INFORMATION:  
; APPLICANT: He, Wei-Wu et al.  
; TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme  
; TITLE OF INVENTION: Like Apoptosis Protease 3 and 4  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Ave.  
; CITY: Rockville  
; STATE: MD  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/462,969B  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/334,251  
; FILING DATE: 11-NOV-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brookes, A. Anders  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PF140P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 301-309-8504  
; TELEFAX: 301-309-8439  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 277 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-462-969B-4

Query Match 100.0%; Score 1463; DB 3; Length 277;  
Best Local Similarity 100.0%; Pred. No. 1,7e-161;  
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENTENSVDKSIKNLEPKIIHGSSEMDGSLDYSYKMDYEMGLCIIINKNFHKSTG 60  
Db 1 MENTENSVDKSIKNLEPKIIHGSSEMDGSLDYSYKMDYEMGLCIIINKNFHKSTG 60  
QY 61 MTSRSGTDVDANLRETFRNKLYEVNRKNDLTREIIVELMRDVSKEDESKSSFCVLLS 120  
Db 61 MTSRSGTDVDANLRETFRNKLYEVNRKNDLTREIIVELMRDVSKEDESKSSFCVLLS 120  
QY 121 HGEGLIFGTNGPVDLKKITNFFRGDRCSLTGPKFLIIQACRGTELDGCIETDSGVD 180  
Db 121 HGEGLIFGTNGPVDLKKITNFFRGDRCSLTGPKFLIIQACRGTELDGCIETDSGVD 180  
QY 181 DMACHKIPVEADFLYASTAGYYSWRNSKDSGSMFIQSLCAMLKQYADKLEFMHILTRVN 240  
Db 181 DMACHKIPVEADFLYASTAGYYSWRNSKDSGSMFIQSLCAMLKQYADKLEFMHILTRVN 240

|||||  
Db 181 DMACHRIPEADFLYASTAPGYISWRNSKDGSMFIOSLCAMLKQYADKLEFPHILTRVN 240  
QY 241 RKVATEFESEFSDATFHAKKOIPCIVSMLTKELEYFH 277  
Db 241 RKVATEFESEFSDATFHAKKOIPCIVSMLTKELEYFH 277

RESULT 4  
US-08-964-313-6  
Sequence 6, Application US/08964313  
Patent No. 6114132

GENERAL INFORMATION:  
APPLICANT: DESMARAIS, SYLVIE  
APPLICANT: FRIESEN, RICHARD  
APPLICANT: GRESSER, MICHAEL  
APPLICANT: KENNEDY, BRIAN  
APPLICANT: NICHOLSON, DONALD  
APPLICANT: RAMACHANDRAN, CHIDAMBARAN  
APPLICANT: SKOREY, KATHRYN  
APPLICANT: FORD-HUTCHINSON, ANTHONY  
TITLE OF INVENTION: PHOSPHATASE BINDING ASSAY  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PHILIPPE L. DURETTE - MERCK & CO., INC.  
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000  
CITY: RAHWAY  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/964, 313  
FILING DATE: 04-NOV-1997  
CLASSIFICATION: 435  
Prior Application DATA:  
APPLICATION NUMBER: 60/030,408  
FILING DATE: 04-NOV-1996  
APPLICATION NUMBER: PCT/CA97/00825  
FILING DATE: 03-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: DURETTE, PHILIPPE L.  
REGISTRATION NUMBER: 35,125  
REFERENCE/DOCKET NUMBER: 19824Y  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-4568  
TELEFAX: 732-594-4720  
TELEX:  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 277 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-964-313-6

Query Match 100.0%; Score 1463; DB 3; Length 277;  
Best Local Similarity 100.0%; Pred. No. 1.7e-161;  
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MENTENSVDSSIKNLEPKIIHGSSEMDGSLDNSYKMDYPEMGLCIIINNNKPFHSTG 60  
Db 1 MENTENSVDSSIKNLEPKIIHGSSEMDGSLDNSYKMDYPEMGLCIIINNNKPFHSTG 60  
QY 61 MTSRSGTDVDAANLRETFRNILKYEVNRKNDLTRREIIVELMRDYSKEDHSKRSSFVCVLLS 120  
Db 61 MTSRSGTDVDAANLRETFRNILKYEVNRKNDLTRREIIVELMRDYSKEDHSKRSSFVCVLLS 120

QY 121 HGESEITGTGPNPVDLKTITNFFRGDRCSLTGKREPLFIIOACRGTELDGCIETDGVDD 180  
Db 121 HGESEITGTGPNPVDLKTITNFFRGDRCSLTGKREPLFIIOACRGTELDGCIETDGVDD 180  
QY 181 DMACHRIPEADFLYASTAPGYISWRNSKDGSMFIOSLCAMLKQYADKLEFPHILTRVN 240  
Db 181 DMACHRIPEADFLYASTAPGYISWRNSKDGSMFIOSLCAMLKQYADKLEFPHILTRVN 240  
QY 241 RKVATEFESEFSDATFHAKKOIPCIVSMLTKELEYFH 277  
Db 241 RKVATEFESEFSDATFHAKKOIPCIVSMLTKELEYFH 277

RESULT 5  
US-09-069-138-6  
Sequence 6, Application US/09069138  
Patent No. 6348572

GENERAL INFORMATION:  
APPLICANT: DESMARAIS, SYLVIE  
APPLICANT: DUFRESNE, CLAUDE  
APPLICANT: FRIESEN, RICHARD  
APPLICANT: LEBLANC, YVES  
APPLICANT: ROY, PATRICK  
APPLICANT: YOUNG, ROBERT N.  
APPLICANT: ZAMBONI, ROBERT  
TITLE OF INVENTION: NEW LIGANDS FOR PHOSPHATASE  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PHILIPPE L. DURETTE - MERCK & CO., INC.  
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000  
CITY: RAHWAY  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Diskette  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/069,138  
FILING DATE: 29-APR-1998  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: DURETTE, PHILIPPE L.  
REGISTRATION NUMBER: 35,125  
REFERENCE/DOCKET NUMBER: 19840Y1A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-4568  
TELEFAX: 732-594-4720  
TELEX:  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 277 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-069-138-6

Query Match 100.0%; Score 1463; DB 4; Length 277;  
Best Local Similarity 100.0%; Pred. No. 1.7e-161;  
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MENTENSVDSSIKNLEPKIIHGSSEMDGSLDNSYKMDYPEMGLCIIINNNKPFHSTG 60  
Db 1 MENTENSVDSSIKNLEPKIIHGSSEMDGSLDNSYKMDYPEMGLCIIINNNKPFHSTG 60  
QY 61 MTSRSGTDVDAANLRETFRNILKYEVNRKNDLTRREIIVELMRDYSKEDHSKRSSFVCVLLS 120  
Db 61 MTSRSGTDVDAANLRETFRNILKYEVNRKNDLTRREIIVELMRDYSKEDHSKRSSFVCVLLS 120

; SEQ ID NO 12 .

PRIOR APPLICATION DATA: ;  
FILING DATE: 27-DEC-; ;



```

: APPLICATION NUMBER: IL 117,932
: FILING DATE: 16-APR-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Browdy, Roger L.
: REGISTRATION NUMBER: 25,618
: REFERENCE/DOCKET NUMBER: WALLACH-19
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 628-5197
: TELEFAX: (202) 737-3528
: INFORMATION FOR SEQ ID NO: 30:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 277 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-983-502-30

Query Match          99.8%; Score 1460; DB 4; Length 277;
Best Local Similarity 99.6%; Pred. No. 3.7e-161;
Matches 276; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENTENSVDKSKIKNLEPKIIHGESMDGSIIDNSYKMDYPEMGLCIINNNKPHKSTG 60
DB 1 MENTENSVDKSKIKNLEPKIIHGESMDGSIIDNSYKMDYPEMGLCIINNNKPHKSTG 60
QY 61 MTSRSGTDVDANLRETFRNLYEVRNKNLDTREIIVELMRDYSKEDHSKRSFVCVLLS 120
DB 61 MTSRSGTDVDANLRETFRNLYEVRNKNLDTREIIVELMRDYSKEDHSKRSFVCVLLS 120
QY 121 HGEGLIIFGTNGPVLDLKITNFFRGDRCSLTGKPKLFIQACRGTELDGGIETDSGVD 180
DB 121 HGEGLIIFGTNGPVLDLKITNFFRGDRCSLTGKPKLFIQACRGTELDGGIETDSGVD 180
QY 181 DMACHRIPEADFLYASTAPAGYSWRNSKDGSMFIQSLCAMLKQYADKLEFMHILTRVN 240
DB 181 DMACHRIPEADFLYASTAPAGYSWRNSKDGSMFIQSLCAMLKQYADKLEFMHILTRVN 240
QY 241 RKVATFESEFSFDPATFHAKKOIPCIIVSMLTRELYFYH 277
DB 241 RKVATFESEFSFDPATFHAKKOIPCIIVSMLTRELYFYH 277

RESULT 9
PCT-US96-10521-30
: Sequence 30, Application PC/TUS9610521
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
: NUMBER OF SEQUENCES: 34
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US96/10521
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: IL 114,615
: FILING DATE: 16-JUL-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: IL 114,986
: FILING DATE: 17-AUG-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: IL 115,319
: FILING DATE: 14-SEP-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: IL 116,588
: FILING DATE: 27-DEC-1995
: PRIOR APPLICATION DATA:
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: APPLICATION NUMBER: IL 117,932
: FILING DATE: 16-APR-1996
: INFORMATION FOR SEQ ID NO: 30:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 277 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: PCT-US96-10521-30

Query Match          99.8%; Score 1460; DB 5; Length 277;
Best Local Similarity 99.6%; Pred. No. 3.7e-161;
Matches 276; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENTENSVDKSKIKNLEPKIIHGESMDGSIIDNSYKMDYPEMGLCIINNNKPHKSTG 60
DB 1 MENTENSVDKSKIKNLEPKIIHGESMDGSIIDNSYKMDYPEMGLCIINNNKPHKSTG 60
QY 61 MTSRSGTDVDANLRETFRNLYEVRNKNLDTREIIVELMRDYSKEDHSKRSFVCVLLS 120
DB 61 MTSRSGTDVDANLRETFRNLYEVRNKNLDTREIIVELMRDYSKEDHSKRSFVCVLLS 120
QY 121 HGEGLIIFGTNGPVLDLKITNFFRGDRCSLTGKPKLFIQACRGTELDGGIETDSGVD 180
DB 121 HGEGLIIFGTNGPVLDLKITNFFRGDRCSLTGKPKLFIQACRGTELDGGIETDSGVD 180
QY 181 DMACHRIPEADFLYASTAPAGYSWRNSKDGSMFIQSLCAMLKQYADKLEFMHILTRVN 240
DB 181 DMACHRIPEADFLYASTAPAGYSWRNSKDGSMFIQSLCAMLKQYADKLEFMHILTRVN 240
QY 241 RKVATFESEFSFDPATFHAKKOIPCIIVSMLTRELYFYH 277
DB 241 RKVATFESEFSFDPATFHAKKOIPCIIVSMLTRELYFYH 277

RESULT 10
US-08-964-308-10
: Sequence 10, Application US/08964308
: Patent No. 6066715
: GENERAL INFORMATION:
: APPLICANT: DESMARAIS, SYLVIE
: APPLICANT: FRIESEN, RICHARD
: APPLICANT: ZAMBONI, ROBERT
: TITLE OF INVENTION: NEW LIGANDS FOR PHOSPHATASE
: NUMBER OF SEQUENCES: 15
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: ROBERT J. NORTH - MERCK & CO., INC.
: STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
: CITY: RAHWAY
: STATE: NJ
: COUNTRY: USA
: ZIP: 07065
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy diskette
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/964,308
: FILING DATE: 04-NOV-1996
: CLASSIFICATION: 530
: ATTORNEY/AGENT INFORMATION:
: NAME: NORTH, ROBERT J.
: REGISTRATION NUMBER: 27,366
: REFERENCE/DOCKET NUMBER: 19840 PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 732-594-7262
: TELEFAX: 732-594-4720
: TELEX:
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
```

LENGTH: 277 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-964-308-10

Query Match 99.3%; Score 1453; DB 3; Length 277;  
Best Local Similarity 99.6%; Pred. No. 2.4e-160;  
Matches 276; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MENTENSVDKSKIKNLEPKIIHSESDSGISLDSYKMDYPMGLCIINNNKFKSTG 60  
DB 1 MENTENSVDKSKIKNLEPKIIHSESDSGISLDSYKMDYPMGLCIINNNKFKSTG 60  
QY 61 MTSRSGTDVAANLRETFNRLKYEVRNKNLDTREIYELMRDYSKEDHSKRSFVCVLLS 120  
DB 61 MTSRSGTDVAANLRETFNRLKYEVRNKNLDTREIYELMRDYSKEDHSKRSFVCVLLS 120  
QY 121 HGEEGIIIFGNGPVDLKKITNFRGDRCSLTGPKLFIIOACRGTELDGIEITDSGVD 180  
DB 121 HGEEGIIIFGNGPVDLKKITNFRGDRCSLTGPKLFIIOACRGTELDGIEITDSGVD 180  
QY 181 DMACHKIPVEADFLYASTAPGYYSWRNSKDSGSMFIOSLCAMLKQYADKLEFMHILTRVN 240  
DB 181 DMACHKIPVEADFLYASTAPGYYSWRNSKDSGSMFIOSLCAMLKQYADKLEFMHILTRVN 240  
QY 241 RKVATEFESESPDATHAKKOIPCIYSMLTKELYFTH 277  
DB 241 RKVATEFESESPDATHAKKOIPCIYSMLTKELYFTH 277

## RESULT 11

US-08-964-313-10  
Sequence 10, Application US/08964313  
Patent No. 6114132

## GENERAL INFORMATION:

APPLICANT: DESMARAIS, SYLVIE  
APPLICANT: FRIESEN, RICHARD  
APPLICANT: GRESSER, MICHAEL  
APPLICANT: KENNEDY, BRIAN  
APPLICANT: NICHOLSON, DONALD  
APPLICANT: RAMACHANDRAN, CHIDAMBARAN  
APPLICANT: SKOREY, KATHRYN  
APPLICANT: FORD-HUTCHINSON, ANTHONY  
TITLE OF INVENTION: PHOSPHATASE BINDING ASSAY  
NUMBER OF SEQUENCES: 15

## CORRESPONDENCE ADDRESS:

ADDRESSEE: PHILIPPE L. DURETTE - MERCK & CO., INC.  
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000  
CITY: RAHWAY  
STATE: NJ  
COUNTRY: USA

ZIP: 07065

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/964,313

FILING DATE: 04-NOV-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/030,408

FILING DATE: 04-NOV-1996

APPLICATION NUMBER: PCT/CA97/00825

FILING DATE: 03-NOV-1996

ATTORNEY/AGENT INFORMATION:

NAME: DURETTE, PHILIPPE L.

REGISTRATION NUMBER: 35,125

REFERENCE/DOCKET NUMBER: 19824Y

TELECOMMUNICATION INFORMATION:

TELEPHONE: 732-594-4568  
TELEFAX: 732-594-4720  
TELEX:  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 277 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-964-313-10

Query Match 99.3%; Score 1453; DB 3; Length 277;  
Best Local Similarity 99.6%; Pred. No. 2.4e-160;  
Matches 276; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MENTENSVDKSKIKNLEPKIIHSESDSGISLDSYKMDYPMGLCIINNNKFKSTG 60  
DB 1 MENTENSVDKSKIKNLEPKIIHSESDSGISLDSYKMDYPMGLCIINNNKFKSTG 60  
QY 61 MTSRSGTDVAANLRETFNRLKYEVRNKNLDTREIYELMRDYSKEDHSKRSFVCVLLS 120  
DB 61 MTSRSGTDVAANLRETFNRLKYEVRNKNLDTREIYELMRDYSKEDHSKRSFVCVLLS 120  
QY 121 HGEEGIIIFGNGPVDLKKITNFRGDRCSLTGPKLFIIOACRGTELDGIEITDSGVD 180  
DB 121 HGEEGIIIFGNGPVDLKKITNFRGDRCSLTGPKLFIIOACRGTELDGIEITDSGVD 180  
QY 181 DMACHKIPVEADFLYASTAPGYYSWRNSKDSGSMFIOSLCAMLKQYADKLEFMHILTRVN 240  
DB 181 DMACHKIPVEADFLYASTAPGYYSWRNSKDSGSMFIOSLCAMLKQYADKLEFMHILTRVN 240  
QY 241 RKVATEFESESPDATHAKKOIPCIYSMLTKELYFTH 277  
DB 241 RKVATEFESESPDATHAKKOIPCIYSMLTKELYFTH 277

## RESULT 12

US-09-069-138-10  
Sequence 10, Application US/09069138  
Patent No. 6348572

## GENERAL INFORMATION:

APPLICANT: DESMARAIS, SYLVIE  
APPLICANT: DUREPSENE, CLAUDE  
APPLICANT: FRIESEN, RICHARD  
APPLICANT: LEBLANC, YVES  
APPLICANT: ROY, PATRICK  
APPLICANT: YOUNG, ROBERT N.  
APPLICANT: ZAMBONI, ROBERT  
TITLE OF INVENTION: NEW LIGANDS FOR PHOSPHATASE  
NUMBER OF SEQUENCES: 15

## CORRESPONDENCE ADDRESS:

ADDRESSEE: PHILIPPE L. DURETTE - MERCK & CO., INC.  
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000  
CITY: RAHWAY  
STATE: NJ  
COUNTRY: USA

ZIP: 07065

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Diskette

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/069,138

FILING DATE: 29-APR-1998

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: DURETTE, PHILIPPE L.

REGISTRATION NUMBER: 35,125

REFERENCE/DOCKET NUMBER: 19840YIA

TELECOMMUNICATION INFORMATION:



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; Sequence 34, Application US/09227721
; Patent No. 6379950
; GENERAL INFORMATION:
; APPLICANT: Alnemi, Ebad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 480140.431
; CURRENT APPLICATION NUMBER: US/09/227,721
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Rev-Caspase-3 constructed from human caspase -3
US-09-227-721-34

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Query Match      62.3%; Score 912; DB 4; Length 290;
Best Local Similarity 100.0%; Pred. No. 1.7e-97;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MENTENSVDKSKTKNLEPKIIHSESDSGISLDSYKMDYPEMGLCIINNNKHFHSTG 60
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DB 116 MENTENSVDKSKTKNLEPKIIHSESDSGISLDSYKMDYPEMGLCIINNNKHFHSTG 175
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 61 MTSRSGTDVDAANLRETFRLKYEVRNKNLDTREIYELMRDYSKEDHSKRSSFVCLLS 120
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 176 MTSRSGTDVDAANLRETFRLKYEVRNKNLDTREIYELMRDYSKEDHSKRSSFVCLLS 235
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 121 HSEGIIFGTNGPVDLKKITNFFRGDRCSLTGKPKLFIIOACRGTELDGCIETD 175
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 236 HGBEGIIIFGTNGPVDLKKITNFFRGDRCSLTGKPKLFIIOACRGTELDGCIETD 290
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Search completed: December 2, 2002, 12:58:44  
 Job time : 12.8948 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 2, 2002, 12:57:12 ; Search time 7.64138 Seconds  
(without alignments)  
577.252 Million cell updates/sec

Title: US-09-895-263-4

Perfect score: 1463

Sequence: 1 MENTENSVDKSIKMLEPKI.....AKQIPCIYSMLTKELFYH 277

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 102317 seqs, 15924203 residues

Total number of hits satisfying chosen parameters: 102317

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications-AA:\*  
1: /cgn2\_6/ptodata/1/pubppaa/US08\_NEW\_PUB.pep:\*  
2: /cgn2\_6/ptodata/1/pubppaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubppaa/US06\_PUBCOMB.pep:\*  
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12: /cgn2\_6/ptodata/1/pubppaa/US10\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/1/pubppaa/US60\_NEW\_PUB.pep:\*  
14: /cgn2\_6/ptodata/1/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1463	100.0	277	10	US-09-895-263-4
2	1460	99.8	277	10	US-09-954-697-12
3	1397	95.5	264	9	US-10-103-448-3
4	912	62.3	290	10	US-09-954-697-34
5	896	61.2	285	10	US-09-954-697-35
6	833	56.9	182	10	US-09-809-905-2
7	725	49.6	303	10	US-09-944-851-2
8	725	49.6	303	10	US-09-954-697-24
9	721	49.3	303	10	US-09-895-263-2
10	525.5	33.9	293	10	US-09-954-697-21
11	429	28.3	476	10	US-09-954-697-27
12	423	28.9	286	10	US-09-862-915-1
13	421	28.8	479	10	US-09-410-194-20
14	421	28.8	496	10	US-09-952-768-4
15	417	28.5	416	9	US-10-068-569-1
16	411	28.1	416	10	US-09-954-697-30
17	376.5	25.7	503	10	US-09-888-243-29
18	374.5	25.6	505	10	US-09-888-243-5
19	372.5	25.5	479	10	US-09-888-243-6

20	349	23.9	479	10	US-09-952-768-2	Sequence 2, Appli
21	349	23.9	479	10	US-09-954-697-33	Sequence 33, Appli
22	343.5	23.5	354	10	US-09-888-243-20	Sequence 20, Appli
23	343.5	23.5	503	10	US-09-888-243-2	Sequence 2, Appli
24	336.5	23.0	451	10	US-09-888-243-28	Sequence 28, Appli
25	328.5	22.5	435	10	US-09-954-697-9	Sequence 9, Appli
26	321	21.9	521	10	US-09-962-834A-2	Sequence 2, Appli
27	321	21.9	571	10	US-09-410-194-21	Sequence 21, Appli
28	316	21.6	167	10	US-09-864-761-48728	Sequence 48728, A
29	294	20.1	300	10	US-09-954-697-36	Sequence 36, Appli
30	274.5	18.8	242	10	US-09-764-803A-24	Sequence 24, Appli
31	274.5	18.8	242	10	US-09-845-028-2	Sequence 2, Appli
32	274.5	18.8	242	10	US-09-845-028-9	Sequence 9, Appli
33	274	18.7	257	10	US-09-764-803A-2	Sequence 2, Appli
34	274	18.7	260	10	US-09-989-903-2	Sequence 2, Appli
35	273.5	18.7	242	10	US-09-989-903-5	Sequence 5, Appli
36	271.5	18.6	229	10	US-09-764-803A-4	Sequence 4, Appli
37	265.5	18.1	410	10	US-09-917-265-24	Sequence 24, Appli
38	259.5	17.7	410	10	US-09-917-265-15	Sequence 15, Appli
39	250	17.1	51	10	US-09-989-903-34	Sequence 34, Appli
40	247.5	16.9	402	10	US-09-888-243-14	Sequence 14, Appli
41	246.5	16.8	377	10	US-09-954-697-15	Sequence 15, Appli
42	244	16.7	58	10	US-09-989-903-27	Sequence 27, Appli
43	240.5	16.4	163	10	US-09-864-761-47950	Sequence 47950, A
44	232.5	15.9	418	10	US-09-954-697-18	Sequence 18, Appli
45	229.5	15.7	214	10	US-09-989-903-9	Sequence 9, Appli

## ALIGNMENTS

RESULT 1  
US-09-895-263-4  
; Sequence 4, Application US/09895263  
; Patent No. US20020076793A1  
GENERAL INFORMATION:  
APPLICANT: He, Wei-Wu et al.  
TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme  
Like Apoptosis Protease 3 and 4  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Ave.  
CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/895,263  
FILING DATE: 02-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: <Unknown>  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Jonathan L. Klein  
REGISTRATION NUMBER: 41,119  
REFERENCE/DOCKET NUMBER: PF140  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-251-6015  
TELEFAX: 301-309-8439  
INFORMATION FOR SEQ ID NO. 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 277 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein



Db 116 MENTENSVDKSKIKNEPKIIHGSSEMSDGSISLDSYKMDYPMGCLCIINNNKFNHKSSTG 175  
QY 61 MTSRSGTDVDAANLRETFRNLYEVNRKNDLTREIYELMRDVSKEHDSKRSFVCVLLS 120  
Db 176 MTSRSGTDVDAANLRETFRNLYEVNRKNDLTREIYELMRDVSKEHDSKRSFVCVLLS 235  
QY 121 HGEEGIIFGTNGPVDLKITNFFRGDRCSLTGKPKLFIIOACRGTELDGCIETD 175  
Db 236 HGEEGIIFGTNGPVDLKITNFFRGDRCSLTGKPKLFIIOACRGTELDGCIETD 290

## RESULT 5

US-09-954-697-35  
Sequence 35, Application US/09954697  
Patent No. US20020106631A1  
GENERAL INFORMATION:  
APPLICANT: Alnemri, Emad S.  
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES  
FILE REFERENCE: 480140.43ID2  
CURRENT FILING DATE: 2001-09-14  
NUMBER OF SEQ ID NOS: 116  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 35  
LENGTH: 285  
TYPE: PRP  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Uncleavable Rev-Caspase-3 constructed from human  
US-09-954-697-35

Query Match 61.2%; Score 896; DB 10; Length 285;  
Best Local Similarity 98.9%; Pred. No. 7.9e-81;  
Matches 173; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MENTENSVDKSKIKNEPKIIHGSSEMSDGSISLDSYKMDYPMGCLCIINNNKFNHKSSTG 60  
Db 111 MENTENSVDKSKIKNEPKIIHGSSEMSDGSISLDSYKMDYPMGCLCIINNNKFNHKSSTG 170  
QY 61 MTSRSGTDVDAANLRETFRNLYEVNRKNDLTREIYELMRDVSKEHDSKRSFVCVLLS 120  
Db 171 MTSRSGTDVDAANLRETFRNLYEVNRKNDLTREIYELMRDVSKEHDSKRSFVCVLLS 230  
QY 121 HGEEGIIFGTNGPVDLKITNFFRGDRCSLTGKPKLFIIOACRGTELDGCIETD 175  
Db 231 HGEEGIIFGTNGPVDLKITNFFRGDRCSLTGKPKLFIIOACRGTELDGCIETD 285

## RESULT 6

US-09-809-905-2  
Sequence 2, Application US/09809905  
Patent No. US2002001806A1  
GENERAL INFORMATION:  
APPLICANT: Huang, Yuanhui  
APPLICANT: Sun, Yi  
TITLE OF INVENTION: CASPASE-35 SPLICING VARIANT  
FILE REFERENCE: U.S. Application A0000224  
CURRENT FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/204,468  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 2  
LENGTH: 182  
TYPE: PRP  
ORGANISM: Homo sapiens  
US-09-809-905-2

Query Match 56.9%; Score 833; DB 10; Length 182;

Best Local Similarity 100.0%; Pred. No. 6.8e-75;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENTENSVDKSKIKNEPKIIHGSSEMSDGSISLDSYKMDYPMGCLCIINNNKFNHKSSTG 60  
Db 1 MENTENSVDKSKIKNEPKIIHGSSEMSDGSISLDSYKMDYPMGCLCIINNNKFNHKSSTG 60  
QY 61 MTSRSGTDVDAANLRETFRNLYEVNRKNDLTREIYELMRDVSKEHDSKRSFVCVLLS 120  
Db 61 MTSRSGTDVDAANLRETFRNLYEVNRKNDLTREIYELMRDVSKEHDSKRSFVCVLLS 120  
QY 121 HGEEGIIFGTNGPVDLKITNFFRGDRCSLTGKPKLFIIO 161  
Db 121 HGEEGIIFGTNGPVDLKITNFFRGDRCSLTGKPKLFIIO 161

## RESULT 7

US-09-944-851-2  
Sequence 2, Application US/09944851  
Patent No. US20020102648A1  
GENERAL INFORMATION:  
APPLICANT: Alnemri, Emad S.  
Fernandes-Alnemri, Teresa  
Litwack, Gerald  
Armstrong, Robert  
Tomasetti, Kevin  
TITLE OF INVENTION: Mch3, A No. US20020102648A1 Apoptotic Protease,  
Nucleic Acids Encoding and Methods of Use  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESS: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/944,851  
FILING DATE: 31-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/556,627  
FILING DATE: 13-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-ID 1813  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 303 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-944-851-2

Query Match 49.6%; Score 725; DB 10; Length 303;  
Best Local Similarity 51.2%; Pred. No. 6.1e-64;  
Matches 145; Conservative 49; Mismatches 77; Indels 12; Gaps 3;

QY 5 ENSVDKSKIK-NLEPKIIHGSSEMSDGSISLDSN-----YKMDYPMGCLCIINNNKFN 55  
Db 19 EDSVDKPKDRSFPVPSLFSKSKKNTVRSIKTTRDVPYQYNNMFKLGCIINNNKFN 78  
QY 56 HKSTGMSRSGTDVDAANLRETFRNLYEVNRKNDLTREIYELMRDVSKEHDSKRSFV 115

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Db      79  D K V T G M G R N T D D A E A L F C F R S L S E F D V I V Y N D C C A K M O D L L K A S E D H T N A C F A 138
QY      116  C Y L L S H G E G I I F C T N G P V D L K R T N F E F G R C S L G K R F L I O A C R E T L D C G E T D 175
Db      139  C I L L S H G E N I Y G K D G T P I K D L A I F R D R C R T L L E K R L F F I O A C R E T L D D G I O A D 198
QY      176  S G V D D D A C --- K I P E A D F L I A Y S T A P G Y S M R N S D S W F I Q S I C A M I K O Y A D K L E F 232
Db      199  S G P I N D D A N R Y K I P E A D L F Y S V P G Y S W R S G R S W F E O A L C S I L E E H G D L E I 258
QY      233  M A I L T R V N R K A Y A T E F E S F E P A T H A R K O I P C I A S M L T K E L Y F 275
Db      259  M Q I L T R V N D R A R H F E S O D P R H E H K O I P C V A S M L T K E L Y F 301

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RESULT 8
US-09-954-697-24
: Sequence 24, Application US/09954697
: Patent No. US20020106631A1
: GENERAL INFORMATION:
: APPLICANT: Alnemri, Emad S.
: TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
: FILE REFERENCE: 480140.431D2
: CURRENT APPLICATION NUMBER: US/09/954, 697
: CURRENT FILING DATE: 2001-09-14
: NUMBER OF SEQ. ID NOS: 116
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ. ID NO. 24
: LENGTH: 303
: TYPE: PRT
: ORGANISM: Homo sapien
: US-09-954-697-24

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Query Match	49.68;	Score 725;	DB 10;	Length 303;
Best Local Similarity	51.28;	Pred. No. 6.1e-64;		
Matches 145;	Conservative 49;	Mismatches 77;	Indels 12;	Gaps 3

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1      STATE: MD
2      COUNTRY: USA
3      ZIP: 20850
4
5      COMPUTER READABLE FORM:
6      MEDIUM TYPE: Floppy disk
7      COMPUTER: IBM PC compatible
8      OPERATING SYSTEM: PC-DOS/MS-DOS
9      SOFTWARE: Patent In Release #1.0, Version #1.30
10
11     CURRENT APPLICATION DATA:
12     APPLICATION NUMBER: US/09/895,263
13     FILING DATE: 02-Jul-2001
14     CLASSIFICATION: <Unknown>
15
16     PRIOR APPLICATION DATA:
17     APPLICATION NUMBER: <Unknown>
18     FILING DATE: <Unknown>
19
20     ATTORNEY/AGENT INFORMATION:
21     NAME: Jonathan L. Klein
22     REGISTRATION NUMBER: 41,119
23     REFERENCE/DOCKET NUMBER: PFL140
24     TELECOMMUNICATION INFORMATION:
25     TELEPHONE: 301-251-6015
26     TELEFAX: 301-309-8439
27
28     INFORMATION FOR SEQ ID NO: 2:
29
30     SEQUENCE CHARACTERISTICS:
31     LENGTH: 303 amino acids
32     TYPE: amino acid
33     STRANDEDNESS: single
34     TOPOLOGY: linear
35
36     MOLECULE TYPE: protein
37
38     SEQUENCE DESCRIPTION: SEQ ID NO: 2:
39     US-09-895-263-2

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Query Match	49.3%	Score 721	DB 10	Length 303
Best Local Similarity	50.9%	Pred. No.	1.5e-63	
Matches 144	Conservative 50	Mismatches 77	Indels 12	Gaps 3

RESULT 9  
 US-09-895-263-2  
 Sequence 2, Application US/09895263  
 Patent No. US20020076793A1  
 GENERAL INFORMATION:  
 APPLICANT: He, Wei-Wu et al.  
 TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme  
 Like Apoptosis Protease 3 and 4  
 NUMBER OF SEQUENCES: 12  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Human Genome Sciences, Inc.  
 STREET: 9410 Key West Ave.  
 CITY: Rockville

```

RESULT 10
US-09-954-697-21
? Sequence 21, Application US/09954697
? Patent No. US20020106631A1
? GENERAL INFORMATION:
? APPLICANT: Alimenti, Emad S.
? TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
? TITLE OF INVENTION: THEREOF
? FILE REFERENCE: 480140.431D2
? CURRENT APPLICATION NUMBER: US/09/954,697
? CURRENT FILING DATE: 2001-09-14
? NUMBER OF SEQ ID NOS: 116
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 21
? LENGTH: 293
? TYPE: PRT

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ORGANISM: Homo sapiens  
us-09-410-194-20

Query Match 28.8%; Score 421; DB 10; Length 479;  
Best Local Similarity 37.8%; Pred. No. 1e-33;  
Matches 102; Conservative 49; Mismatches 91; Indels 28; Gaps 8;

QY 24 SESMDGSLDMSYKMDYEMGICITIIINKNFHKST-----GMTSRSGTDVDAANLRE 76  
DB 217 SESQ-----TLDKYQMKSRPGYCLIIINNNHFAKAREKVPKLSIRDRNGTHLDAGALLT 272  
QY 77 TFRNLKYEVRNKNDLTREETVELMRDVSKEHDSKSSFCVLLSHGEGIIFTGNG-PVD 135  
DB 273 TFEELHFEIKPHDDCTVEQIYEILKIYOLMDHSMDCFCICILSHGDKGIITGDOGEAP 332  
QY 136 LKKTINFEPRDRSLTGKPKLFIIOACRGTELDGCI--ETDSG-----VDDMACHK--- 186  
DB 333 IYELTSQFTGLKCPSLAGKPKVFFIOACQGDNYOKGIPVETDSEOPYLEMDLSSPQTRY 392  
QY 187 IPEADFLVAYSTAPGYSWRNSKDSGSMFTIOSLCAMLKQYADK-LEPMHILTRVNRKVA 245  
DB 393 IPDEADFLGMATVNNVCYRNPAEGTWYIOSLCOSLRRCRPGDDILITLITVEVNEVSN 452  
QY 246 EFESFSDATFHAKKQIPCTIVSMITKELYF 275  
DB 453 K-----DDKKNMGKOMPQPTFLRKLVF 476

RESULT 14  
US-09-952-768-4

; Sequence 4, Application US/09952768  
; Patent No. US20020035242A1  
; GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.  
Fernandes-Alnemri, Teresa  
Litwack, Gerald  
Armstrong, Robert  
Tomasselli, Kevin

TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE.

NUMBER OF SEQUENCES: 75

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed Intellectual Property Law Group

STREET: Suite 6300, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/952,768

FILING DATE: 10-Sep-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Christensen, William T.

REGISTRATION NUMBER: 44,614

REFERENCE/DOCKET NUMBER: 480140.424C4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 496 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-952-768-4

Query Match 28.8%; Score 421; DB 10; Length 496;  
Best Local Similarity 37.8%; Pred. No. 1.1e-33;  
Matches 102; Conservative 49; Mismatches 91; Indels 28; Gaps 8;

QY 24 SESMDGSLDMSYKMDYEMGICITIIINKNFHKST-----GMTSRSGTDVDAANLRE 76  
DB 234 SESQ-----TLDKYQMKSRPGYCLIIINNNHFAKAREKVPKLSIRDRNGTHLDAGALLT 289  
QY 77 TFRNLKYEVRNKNDLTREETVELMRDVSKEHDSKSSFCVLLSHGEGIIFTGNG-PVD 135  
DB 290 TFEELHFEIKPHDDCTVEQIYEILKIYOLMDHSMDCFCICILSHGDKGIITGDOGEAP 349  
QY 136 LKKTINFEPRDRSLTGKPKLFIIOACRGTELDGCI--ETDSG-----VDDMACHK--- 186  
DB 350 IYELTSQFTGLKCPSLAGKPKVFFIOACQGDNYOKGIPVETDSEOPYLEMDLSSPQTRY 409  
QY 187 IPEADFLVAYSTAPGYSWRNSKDSGSMFTIOSLCAMLKQYADK-LEPMHILTRVNRKVA 245  
DB 410 IPDEADFLGMATVNNVCYRNPAEGTWYIOSLCOSLRRCRPGDDILITLITVEVNEVSN 469  
QY 246 EFESFSDATFHAKKQIPCTIVSMITKELYF 275  
DB 470 K-----DDKKNMGKOMPQPTFLRKLVF 493

RESULT 15  
US-10-068-569-1

; Sequence 1, Application US/10068569  
; Patent No. US20020160975A1  
; GENERAL INFORMATION:

APPLICANT: Stinivasula, Stinivasa M.  
Fernandes-Alnemri, Teresa  
Litwack, Gerald  
Armstrong, Robert  
Tomasselli, Kevin

TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN  
FILE REFERENCE: 480140.475  
CURRENT APPLICATION NUMBER: US/10/068,569  
CURRENT FILING DATE: 2002-02-06  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 1

LENGTH: 416

TYPE: PRT

ORGANISM: Homo sapiens

US-10-068-569-1

Query Match 28.5%; Score 417; DB 9; Length 416;  
Best Local Similarity 33.2%; Pred. No. 2.1e-33;  
Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;

QY 34 DMSYKMDYEMGICITIIINKNFHKSTGMTSRSGTDVDAANLRETFRNLYEVRNKNDLTR 93  
DB 150 DLAITLSMEPCGHCLIIINNVNFCRESGLTRTGSNIDCEKLRFRFSLHFMVEYKGDTRA 209  
QY 94 EIVELMRDVSKEHDSKSSFCVLLSHGEE-----GIITGNG-PVDLKRITNFFRG 145  
DB 210 KKMVALLELAQODHGALDCCVAVILSHGQASHLOFPAVAVGTGDCPVSEKIVNIFNG 269  
QY 146 DRCRLTGKPKLFIIOACRGTELDGCIETDSGVDDM----- 182  
DB 270 TSCPSLGGPKLFIIOACRGTELDGCIETDSGVDDM----- 182  
QY 183 -ACHRIPEADFLVAYSTAPGYSWRNSKDSGSMFTIOSLCAMLKQYADK-LEPMHILTRVNR 241  
DB 330 DAISLPLTPSDIFVSYSTFGVSWRDRSGSMVYETLDDITFEQNAHSDLOSLLIRVAN 389  
QY 242 KVATEFESFSDATFHAKKQIPCTIVSMITKELYF 275  
DB 390 AVSVK-----GIYKMGKCNFPLRKKLVF 413

Search completed: December 2, 2002, 13:04:19  
Job time : 8.64138 secs





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FT Region 176..193
FT /note= "amino-terminal sequence determined for
FT purified enzyme subunits"
FT Region 161..165
FT /note= "conserved pentapeptide containing putative
FT catalytic cysteine"
FT Protein 176..277
FT /note= "12 kDa subunit p12"
PN MO9633268-A1.
XX
XX
PD 24-OCT-1996.
XX
XX
PF 17-APR-1996; 96WO-US05282.
XX
XX
PR 21-APR-1995; 95US-0426557.
XX
XX
PA (MER1 ) MERCK & CO INC.
XX (MER1 ) MERCK FROST CANADA INC.
XX
XX
PI All A, Miller DK, Nicholson DW, Thornberry NA, Vallancourt JP;
XX WPI; 1996-48575/48.
XX
XX
PS Claim 1; Fig 4C; 84pp; English.
XX
XX
CC The present sequence is the CPP23beta or Glu190 isoform of the
CC inactive CPP32 proenzyme (a member of the interleukin converting
CC enzyme/pro-apoptotic protein CED-3 family of cysteine proteases of
CC unknown function cloned from Jurkat cells), the proteolytic product
CC of which is the poly(DP-ribose) polymerase (PARP) protease.
CC
CC The PARP cleavage enzyme was purified from the human
CC monocytic leukemia cell line, THP-1, using standard ion exchange
CC chromatography techniques and SDS PAGE. Apopain can be used to
CC identify apopain activity modulators, while apopain encoding DNA
CC may be used for apopain production or in gene therapy (i.e. in vivo
CC or ex vivo gene transplantation) for enhancing the pro-inflammatory
CC or pro-apoptotic effects of apopain. Anti-apopain antibodies and
CC antisense DNA can be used to reduce or eliminate the
CC pro-inflammatory or pro-apoptotic effects of apopain. Modulation
CC of apopain activity is beneficial in the treatment of immune,
CC disease, pathogenic infections, cardiovascular and neurological
CC injury, alopecia, ageing, cancer, type I diabetes and Parkinson's
CC and Alzheimer's disease.
XX
XX
SO Sequence 277 AA:
Query Match 100.0%; Score 1463; DB 17; Length 277;
Best Local Similarity 100.0%; Pred. No. 1e-147;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 MENTENSVDKSIKLEKRIIIGSESMDGSLDINSYKMDYPMGICITIIKNNFKRSTG 60
Db 1 MENTENSVDKSIKLEKRIIIGSESMDGSLDINSYKMDYPMGICITIIKNNFKRSTG 60
Oy 61 MTSRSGTDVDAANLRETFRNKLYEVNRKNDLTREIVELMRVSKDHSKRSSFVCVLLS 120
Db 61 MTSRSGTDVDAANLRETFRNKLYEVNRKNDLTREIVELMRVSKDHSKRSSFVCVLLS 120
Oy 121 HGEEGIIIFGTNGPVDLKTITNFFRGDRCSLTGKPKLFTIOACRGTELDGCIETSGVDD 180
Db 121 HGEEGIIIFGTNGPVDLKTITNFFRGDRCSLTGKPKLFTIOACRGTELDGCIETSGVDD 180
Oy 181 DMACHKRIPEADFLIAYSTAPGYISWRNSKDGSMFIQSLCAMLKQYADKLEFMHILITRVN 240
Db 181 DMACHKRIPEADFLIAYSTAPGYISWRNSKDGSMFIQSLCAMLKQYADKLEFMHILITRVN 240
Oy 241 RKVATEFESFSDATFPAKKQIPCIIVSMLTKELYFYH 277

```

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Db 241 RKVATEFESFSDATFPAKKQIPCIIVSMLTKELYFYH 277
RESULT 2
ID AAM00677 standard; Protein; 277 AA.
XX
XX AAM00677;
XX
XX AC AAM00677;
XX
XX DT 06-DEC-1996 (first entry)
XX
XX DE Pro-Yama.
XX
XX KM Yama; CrmA; apoptosis; Fas receptor; T-lymphocyte; AIDS; HIV;
XX human immunodeficiency virus.
XX
XX OS Homo sapiens.
XX
XX PN WO9625501-A2.
XX
XX PD 22-AUG-1996.
XX
XX
XX PF 09-FEB-1996; 96WO-US01882.
XX
XX PR 01-JUN-1995; 95US-0457731.
XX PR 13-FEB-1995; 95US-0389812.
XX
XX PA (UNMT ) UNIV MICHIGAN.
XX
XX
XX PI Dixit VM;
XX
XX DR WPI; 1996-393402/39.
XX N-PSDB; AAT33567.
XX
XX
XX PT New nucleic acid encoding Yama protein or CrmA mutant - useful for
XX modulating apoptosis, maintaining T cell viability in AIDS patients
XX and for drug screening
XX
XX PS Disclosure; Fig 1; 118pp; English.
XX
XX
XX CC Human pro-Yama (AAM00677) is a zymogen which upon activation cleaves
XX PARP to an 85 kDa form. Activated Yama has the ability to modulate
XX cellular function associated with the Fas receptor pathway such as
XX Fas-associated apoptosis. This activity is inhibited by CrmA (see
XX also AAM00678). The pro-Yama sequence was deduced from a cDNA clone
XX isolated from human umbilical vein endothelial cells. Yama can be
XX produced in a host cell and used to modulate cellular function, to
XX raise antibodies, or to screen for agents or drugs which modulate
XX a Fas-related function such as apoptosis.
XX
XX
XX SO Sequence 277 AA:
Query Match 100.0%; Score 1463; DB 17; Length 277;
Best Local Similarity 100.0%; Pred. No. 1e-147;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 MENTENSVDKSIKLEKRIIIGSESMDGSLDINSYKMDYPMGICITIIKNNFKRSTG 60
Db 1 MENTENSVDKSIKLEKRIIIGSESMDGSLDINSYKMDYPMGICITIIKNNFKRSTG 60
Oy 61 MTSRSGTDVDAANLRETFRNKLYEVNRKNDLTREIVELMRVSKDHSKRSSFVCVLLS 120
Db 61 MTSRSGTDVDAANLRETFRNKLYEVNRKNDLTREIVELMRVSKDHSKRSSFVCVLLS 120
Oy 121 HGEEGIIIFGTNGPVDLKTITNFFRGDRCSLTGKPKLFTIOACRGTELDGCIETSGVDD 180
Db 121 HGEEGIIIFGTNGPVDLKTITNFFRGDRCSLTGKPKLFTIOACRGTELDGCIETSGVDD 180
Oy 181 DMACHKRIPEADFLIAYSTAPGYISWRNSKDGSMFIQSLCAMLKQYADKLEFMHILITRVN 240
Db 181 DMACHKRIPEADFLIAYSTAPGYISWRNSKDGSMFIQSLCAMLKQYADKLEFMHILITRVN 240

```

OY 241 RKVATEFESFSDATFHAKKQIPCIYSLTKELFYH 277  
DB 241 RKVATEFESFSDATFHAKKQIPCIYSLTKELFYH 277

RESULT 3  
AAR95831  
ID AAR95831 standard; Protein; 277 AA.

AC AAR95831;  
DT 28-OCT-1996 (first entry)

DE Human interleukin-1-converting enzyme-like apoptosis protease-4.  
XX IGE-LAP-4; interleukin-1-converting enzyme-like apoptosis protease;  
XX enzyme; Alzheimer's disease; Parkinson's disease; septic shock;  
XX head injury; rheumatoid arthritis.

OS Homo sapiens.

PN W09613603-A1.

PD 09-MAY-1996.

PF 06-JUN-1995; 95WO-US07235.

PR 01-NOV-1994; 94US-0334251.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Hastings GA, He W, Hudson PL, Rosen CA;

DR WPI; 1996-239509/24.

DR N-PSDB; AAT15277.

PT Human ICE-LAP-3 and -4 DNA and protein - useful in the diagnosis  
PT and treatment of Alzheimer's disease, Parkinson's disease,  
PT rheumatoid arthritis, septic shock and head injury

PS Claim 1: Page 44; 67pp; English.

CC This ICE-LAP-4 protein may be used therapeutically, e.g. as an  
CC antitumor or antiviral agent and to control embryonic development  
CC and tissue homeostasis. The protein can also be used to treat  
CC immunosuppression disorders, such as AIDS, by targeting virus  
CC infected cells for cell death. The DNA may find use in gene  
CC therapy applications.

XX Sequence 277 AA:

Query Match 100.0%; Score 1463; DB 17; Length 277;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MENTENSVDKSKIKNLEPKIIHGESMDSGISLDNSYKMDYPMGLCIITNNKMFHSTG 60  
DB 1 MENTENSVDKSKIKNLEPKIIHGESMDSGISLDNSYKMDYPMGLCIITNNKMFHSTG 60

OY 61 MTSRSGTDVDAANLRETFNKLKYEVANKNDLTREIYELMDRVSKEDHSKRSSFVCVLLS 120  
DB 61 MTSRSGTDVDAANLRETFNKLKYEVANKNDLTREIYELMDRVSKEDHSKRSSFVCVLLS 120

OY 121 HGEEGIIIFGTNGPVDLKKITNFFRGDRCSLTGKPKLFITIOACRGTELDGCIETDSGVD 180  
DB 121 HGEEGIIIFGTNGPVDLKKITNFFRGDRCSLTGKPKLFITIOACRGTELDGCIETDSGVD 180

OY 181 DMACHKIPVADFLYAYSTAPGYYSWRNSKDGSMFIOSLCAMLKQYADKLEFMIILTRVN 240  
DB 181 DMACHKIPVADFLYAYSTAPGYYSWRNSKDGSMFIOSLCAMLKQYADKLEFMIILTRVN 240

OY 241 RKVATEFESFSDATFHAKKQIPCIYSLTKELFYH 277  
DB 241 RKVATEFESFSDATFHAKKQIPCIYSLTKELFYH 277

DB 241 RKVATEFESFSDATFHAKKQIPCIYSLTKELFYH 277

RESULT 4  
AAM41688  
ID AAM41688 standard; Protein; 277 AA.

AC AAM41688;  
DT 02-JUL-1998 (first entry)

DE Amino acid sequence of a protein designated YAMA.

XX CrmA; tumour necrosis factor receptor; TNF-R; U1-70; inhibition;  
XX apoptosis; activation; U1-70 path; apoptosis path; identification;  
XX modulation.

OS Synthetic.

PN JP09299077-A.

PD 25-NOV-1997.

PF 27-JAN-1997; 97JP-0012932.

PR 09-FEB-1996; 96US-0591605.

PA (UNMI) UNIV MICHIGAN.

DR WPI; 1996-056551/06.

DR N-PSDB; AAV05471.

PT Controlling apoptosis by inhibiting activation of the U1-70 pathway  
PT - by introduction of nucleic acid encoding protein with CrmA  
PT biological activity into the cell

PS Disclosure; Fig 2; 48pp; Japanese.

CC The present sequence represents a non-naturally occurring protein  
CC designated YAMA. The specification describes a novel method of  
CC controlling cell functions controlled by the tumour necrosis factor  
CC receptor (TNF-R) pathway containing U1-70. The method comprises  
CC introducing a nucleic acid molecule encoding CrmA into a cell, and  
CC culturing the cell under suitable conditions for transcription and  
CC translation of the CrmA nucleic acid. Method for preventing and  
CC inhibiting apoptosis by inhibiting activation of the U1-70 path,  
CC identifying the chemical related to the apoptosis path, and screening a  
CC candidate chemical having biological function in the apoptosis path are  
CC also described. The methods can be used to identify substances which  
CC modulate apoptosis in cells controlled by the TNF-R pathway.

XX Sequence 277 AA:

Query Match 100.0%; Score 1463; DB 19; Length 277;  
Best Local Similarity 100.0%; Pred. No. 1e-147;  
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MENTENSVDKSKIKNLEPKIIHGESMDSGISLDNSYKMDYPMGLCIITNNKMFHSTG 60

OY 61 MTSRSGTDVDAANLRETFNKLKYEVANKNDLTREIYELMDRVSKEDHSKRSSFVCVLLS 120  
DB 61 MTSRSGTDVDAANLRETFNKLKYEVANKNDLTREIYELMDRVSKEDHSKRSSFVCVLLS 120

OY 121 HGEEGIIIFGTNGPVDLKKITNFFRGDRCSLTGKPKLFITIOACRGTELDGCIETDSGVD 180  
DB 121 HGEEGIIIFGTNGPVDLKKITNFFRGDRCSLTGKPKLFITIOACRGTELDGCIETDSGVD 180

OY 181 DMACHKIPVADFLYAYSTAPGYYSWRNSKDGSMFIOSLCAMLKQYADKLEFMIILTRVN 240  
DB 181 DMACHKIPVADFLYAYSTAPGYYSWRNSKDGSMFIOSLCAMLKQYADKLEFMIILTRVN 240

QY 241 RKVATFESEFDPATFHAQQIPCIYSMLTKELYFH 277  
 DB 241 RKVATFESEFDPATFHAQQIPCIYSMLTKELYFH 277

RESULT 5  
 AAM16600  
 ID AAM16600 standard; protein; 277 AA.  
 XX  
 AC AAM16600;  
 XX  
 DT 26-JUN-1997 (first entry)  
 XX  
 DE Apopain CPP32a proenzyme.  
 XX  
 KM CPP32a; isoform; inactive; CPP32; proenzyme; cysteine; protease;  
 KM proteolytic product; poly(DP-ribose) polymerase; PARP; apopain;  
 KM cleavage enzyme; human; monocytic leukaemia; cell line; THP-1;  
 KM identification; modulator; recombinant production; gene therapy;  
 KM pro-inflammatory; pro-apoptotic; apoptosis; inflammation; antibody;  
 KM antisense DNA; treatment; immune; proliferation; degeneration;  
 KM disease; AIDS; acquired immunodeficiency syndrome; autoimmune;  
 KM pathogenic infection; cardiovascular; neurological; injury;  
 KW alopecia; ageing; cancer; type I diabetes; Parkinson's;  
 KM Alzheimer's.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FH Domain  
 FT Location/Qualifiers  
 FT 1..28  
 FT /note= "amino-terminal pro-domain"  
 FT 28..29  
 FT /note= "amino-terminal sequence determined for  
 FT Region  
 FT 29..46  
 FT /note= "amino-terminal sequence determined for  
 FT protein  
 FT 29..175  
 FT /note= "17 kDa subunit p17"  
 FT 175..176  
 FT /note= "176..193  
 FT Region  
 FT 176..193  
 FT /note= "amino-terminal sequence determined for  
 FT Region  
 FT 161..165  
 FT /note= "conserved pentapeptide containing putative  
 FT protein  
 FT 176..277  
 FT /note= "12 kDa subunit p12"  
 XX  
 PN W09633268-A1.  
 XX  
 PD 24-OCT-1996.  
 XX  
 PE 17-APR-1996; 96WO-US05282.  
 XX  
 PR 21-APR-1995; 95US-0426557.  
 XX  
 PA (MERI ) MERCK & CO INC.  
 PA (MERI ) MERCK FROST CANADA INC.  
 XX  
 PI All A, Miller DK, Nicholson DW, Thornberry NA, Vaillancourt JP;  
 DR WPI; 1996-485775/48.  
 XX  
 PT Apopain, a new human apoptosis related enzyme - responsible for the  
 PT proteolytic breakdown of poly(ADP-ribose) polymerase (PARP) which  
 PT occurs at the onset of apoptosis  
 XX  
 PS Claim 1; Page -: 84pp; English.  
 XX  
 CC The present sequence is the CPP32a or Asp190 isoform of the  
 CC inactive CPP32 proenzyme (a member of the interleukin converting  
 CC enzyme/pro-apoptotic protein CED-3 family of cysteine proteases of  
 CC unknown function cloned from Jurkat cells), the proteolytic product  
 CC of which is the poly(DP-ribose) polymerase (PARP) protease,

CC apopain. The PARP cleavage enzyme was purified from the human  
 CC monocytic leukemia cell line, THP-1, using standard ion exchange  
 CC chromatography techniques and SDS PAGE. Apopain can be used to  
 CC identify apopain activity modulators, while apopain encoding DNA  
 CC may be used for apopain production or in gene therapy (i.e. in vivo  
 CC or ex vivo gene transplantation) for enhancing the pro-inflammatory  
 CC or pro-apoptotic effects of apopain. Anti-apopain antibodies and  
 CC antisense DNA can be used to reduce or eliminate the  
 CC pro-inflammatory or pro-apoptotic effects of apopain. Modulation  
 CC of apopain activity is beneficial in the treatment of immune,  
 CC proliferative and degenerative diseases, e.g. AIDS, autoimmune  
 CC disease, pathogenic infections, cardiovascular and neurological  
 CC injury, alopecia, ageing, cancer, type I diabetes and Parkinson's  
 CC and Alzheimer's disease.  
 XX  
 SQ Sequence 277 AA;  
 XX  
 Query Match 99.8%; Score 1460; DB 17; Length 277;  
 Best Local Similarity 99.6%; Pred. No. 2.2e-147;  
 Matches 276; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MENTENSVDKSKIKNEPKIHGSESDSGISLDNSYKMDYPEKGLCIINNNKFKSTG 60  
 DB 1 MENTENSVDKSKIKNEPKIHGSESDSGISLDNSYKMDYPEKGLCIINNNKFKSTG 60  
 QY 61 MTSRSGTDVDAANLRETFRLKTEVRNKNKNDLTREBEIVELMRDYSKEDHSRSSFVCLLS 120  
 DB 61 MTSRSGTDVDAANLRETFRLKTEVRNKNKNDLTREBEIVELMRDYSKEDHSRSSFVCLLS 120  
 QY 121 HGEGLIIFGTNGPVDLKTITNFRGDRCSLTGKPKLFIIOACRGTELDGIEFDSGVDD 180  
 DB 121 HGEGLIIFGTNGPVDLKTITNFRGDRCSLTGKPKLFIIOACRGTELDGIEFDSGVDD 180  
 QY 181 DMACHKIPVADDFLAVYSTAPGYYSWRNSKDSGSMFTIOSLCAMLKQYADKLEFPHILTRVN 240  
 DB 181 DMACHKIPVADDFLAVYSTAPGYYSWRNSKDSGSMFTIOSLCAMLKQYADKLEFPHILTRVN 240  
 QY 241 RKVATFESEFDPATFHAQQIPCIYSMLTKELYFH 277  
 DB 241 RKVATFESEFDPATFHAQQIPCIYSMLTKELYFH 277

RESULT 6  
 AAM21717  
 ID AAY21717 standard; protein; 277 AA.  
 XX  
 AC AAY21717;  
 XX  
 DT 10-SEP-1999 (first entry)  
 XX  
 DE Amino acid sequence of caspase-3 (CPP32).  
 XX  
 DE Rev-caspase; cysteine protease; zymogen; caspase; cancer; gene therapy;  
 KM autoimmune disease; caspase-mediated apoptosis; neurodegenerative;  
 KM tumour cell; myocardial infarction; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W09935277-A2.  
 XX  
 PD 15-JUL-1999.  
 XX  
 PE 11-JAN-1999; 99WO-US00632.  
 XX  
 PR 09-JAN-1998; 98US-0070987.  
 XX  
 PA (UYJE-) UNIV JEFFERSON THOMAS.  
 XX  
 PI Alnemri ES;  
 XX  
 DR WPI; 1999-419353/35.  
 DR N-FSDB; AAX81219.  
 XX

PT New isolated nucleic acid molecule encoding a rev-caspase - used  
PT for screening and identifying inhibitors or enhancers for treating  
PT cancer or autoimmune disease  
XX  
PS Disclosure; Fig 13A-B; 74pp; English.  
XX  
CC The invention relates to nucleic acid molecules encoding rev-caspases.  
CC Rev-caspases are cysteine proteases that specifically cleave proteins  
CC after Asp residues and is expressed as a zymogen, in which the small  
CC subunit is N-terminal to a large subunit. A gene delivery vehicle  
CC comprising a rev-caspase coding sequence is useful for the treatment of  
CC cancer, where the gene delivery vehicle is internalised by tumour cells.  
CC The gene delivery vehicle can also be used to treat autoimmune diseases.  
CC Cells transfected with a rev-caspase expressing vector can be used in  
CC identification of inhibitors or enhancers of caspase-mediated apoptosis.  
CC In vitro translated rev-caspase can be used to identify an inhibitor or  
CC enhancer of caspase processing activity. Caspase inhibitors are useful  
CC for treating neurodegenerative diseases as well as for inhibiting  
CC apoptosis in the heart following myocardial infarction. Sequences  
CC AA81217-AA81226 represent human caspase genes encoding caspase 1-10  
CC gene products (AA81217-81226).  
XX  
SQ Sequence 277 AA:  
Query Match 99.8%; Score 1460; DB 20; Length 277;  
Best Local Similarity 99.6%; Pred. No. 2.2e-147;  
Matches 276; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 MENTENSVDKSKINLEPKIIGSESMDSGISLDSYKMDYPMGLCTIINNNKPKSTG 60  
DB 1 MENTENSVDKSKINLEPKIIGSESMDSGISLDSYKMDYPMGLCTIINNNKPKSTG 60  
OY 61 MTSRSGTDVDANLRETFRNKLYEVNRKNDLTREIIVELMDVSKEDHSKRSSFVCVLLS 120  
DB 61 MTSRSGTDVDANLRETFRNKLYEVNRKNDLTREIIVELMDVSKEDHSKRSSFVCVLLS 120  
OY 121 HGEEGIIIFGTNGPVDLKKTITNFFRGDRCSLTGKPKFLIIQACRGTELDGCIETDGVDD 180  
DB 121 HGEEGIIIFGTNGPVDLKKTITNFFRGDRCSLTGKPKFLIIQACRGTELDGCIETDGVDD 180  
OY 181 DMACHKIPVADDFLYASTAGYYSWRNSKDGSMFIOSLCAMLKQYADKLEFMHILTRYN 240  
DB 181 DMACHKIPVADDFLYASTAGYYSWRNSKDGSMFIOSLCAMLKQYADKLEFMHILTRYN 240  
OY 241 RKVATEFESFSDATFPAKKOIPCIIVSMLTKELYFYH 277  
DB 241 RKVATEFESFSDATFPAKKOIPCIIVSMLTKELYFYH 277  
RESULT 7  
AAU05394  
ID AAU05394 standard; Protein; 277 AA.  
XX  
AC AAU05394;  
XX  
DT 24-OCT-2001 (first entry)  
XX  
DE Human caspase 3.  
XX  
XX Human; caspase 3; apoptosis; hyperproliferative disorder; hepatitis;  
KW viral infection; haematopoietic disorder; autoimmune disorder;  
KW atherosclerosis; neurological disorder.  
XX  
OS Homo sapiens.  
XX  
XX WO200153310-A1.  
XX  
XX 26-JUL-2001.  
XX  
XX 11-JAN-2001; 2001WO-US00888.  
XX  
XX 18-JAN-2000; 2000US-0484617.  
XX

PA (ISIS-) ISIS PHARM INC.  
XX  
XX Zhang H, Cowser LM;  
XX  
XX WPI: 2001-442252/47.  
XX  
XX N-PSDB: AAS10503.  
XX  
XX New antisense compound to inhibit caspase 3 is useful for treating  
PT hepatitis and atherosclerosis -  
XX  
PS Disclosure; Page 92-94; 127pp; English.  
XX  
XX The present sequence representing human caspase 3 is described  
CC in an invention relating to novel antisense oligonucleotides  
CC (AAS10517-AAS10676) and methods of using these compounds for the  
CC modulation of caspase 3 expression. The caspase 3 antisense  
CC oligonucleotides specifically hybridise with and inhibit the  
CC expression of caspase 3. Antisense compounds targeted to caspase 3  
CC are useful to inhibit caspase 3 expression in cells or tissues and  
CC to modulate apoptosis. The caspase 3 antisense oligonucleotides are  
CC useful for treating disorders associated with expression of caspase 3.  
CC Such disorders include hyperproliferative disorders (e.g. cancer),  
CC viral infections (e.g. hepatitis), haematopoietic disorders, autoimmune  
CC disorders, atherosclerosis and neurological disorders (e.g. Alzheimer's  
CC disease).  
XX  
SQ Sequence 277 AA:  
Query Match 99.8%; Score 1460; DB 22; Length 277;  
Best Local Similarity 99.6%; Pred. No. 2.2e-147;  
Matches 276; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 MENTENSVDKSKIKMLPEKIIHGESMDSGISLDSYKMDYPMGLCTIINNNKPKSTG 60  
DB 1 MENTENSVDKSKIKMLPEKIIHGESMDSGISLDSYKMDYPMGLCTIINNNKPKSTG 60  
OY 61 MTSRSGTDVDANLRETFRNKLYEVNRKNDLTREIIVELMDVSKEDHSKRSSFVCVLLS 120  
DB 61 MTSRSGTDVDANLRETFRNKLYEVNRKNDLTREIIVELMDVSKEDHSKRSSFVCVLLS 120  
OY 121 HGEEGIIIFGTNGPVDLKKTITNFFRGDRCSLTGKPKFLIIQACRGTELDGCIETDGVDD 180  
DB 121 HGEEGIIIFGTNGPVDLKKTITNFFRGDRCSLTGKPKFLIIQACRGTELDGCIETDGVDD 180  
OY 181 DMACHKIPVADDFLYASTAGYYSWRNSKDGSMFIOSLCAMLKQYADKLEFMHILTRYN 240  
DB 181 DMACHKIPVADDFLYASTAGYYSWRNSKDGSMFIOSLCAMLKQYADKLEFMHILTRYN 240  
OY 241 RKVATEFESFSDATFPAKKOIPCIIVSMLTKELYFYH 277  
DB 241 RKVATEFESFSDATFPAKKOIPCIIVSMLTKELYFYH 277  
RESULT 8  
AAE00600  
ID AAE00600 standard; Protein; 277 AA.  
XX  
AC AAE00600;  
XX  
XX 02-JUL-2001 (first entry)  
XX  
XX Human caspase-3.  
XX  
XX Human; caspase-3; CPP32; yama; apopain;  
KW cysteine protease; apoptosis; caspase expression cassette; metastasis;  
KW tumour; cathepsin B; urokinase; proliferation; gene therapy.  
XX  
XX Homo sapiens.  
XX  
XX  
XX Key Location/Qualifiers  
FH Cleavage-site 9..10  
FT /label- Proteolytic\_cleavage\_site  
FT Cleavage-site 28..29  
XX



/label= Proteolytic-cleavage-site

FT XX W0200129232-A2.  
PN XX  
XX 26-APR-2001.  
PD XX  
XX 19-OCT-2000; 2000MO-US28941.  
PF XX  
XX 20-OCT-1999; 99US-0160559.  
PR XX 14-AUG-2000; 2000US-0225564.  
XX  
PA (SCIO-) SCIOS INC.  
XX  
PI Cordell B, Li Y;  
XX WPI; 2001-290920/30.  
DR N-PSDB; AAD03910.  
XX  
PT Novel fusion polypeptide comprising first and second caspase subunit  
PT separated by cleavage site not associated in nature with caspase  
PT subunit, useful for cloning gene encoding enzymes involved in  
PT proteolytic cleavage  
XX  
PS Claim 5; Fig 6; 116pp; English.

CC The present amino acid sequence is human Caspase-3 also known as  
CC CPP32, yama and apopain. Caspases are a family of cysteine proteases,  
CC that participate in the initiation and execution of apoptosis. Caspases  
CC exist as pro-enzymes, activated by cleavage into a large and small  
CC subunit, occurring after specific aspartic acid residues within the  
CC pro-enzyme sequence. The present invention relates to a method for  
CC functional cloning of genes encoding proteins or enzymes involved in  
CC proteolytic cleavage. The invention is based on the use of caspase  
CC expression cassettes comprising the coding sequence of a proteolytic  
CC cleavage site flanked by sequences encoding two caspase subunits. A  
CC fusion polypeptide comprising a first and a second caspase subunit,  
CC separated by a cleavage site not associated in nature, is useful for  
CC cloning gene encoding enzymes involved in proteolytic cleavage. An  
CC expression cassette containing fusion polypeptide is used to identify a  
CC mutant cell line deficient in an enzyme of interest and is also useful  
CC for diagnosis and suppression of proliferation or metastases of a tumour  
CC cell characterised by overexpression of a polypeptide (e.g. Cathepsin B  
CC or urokinase, selectively expressed in the tumour cells). DNA encoding  
CC fusion polypeptide is used in gene therapy.  
XX

SQ Sequence 277 AA;

Query Match 99.8%; Score 1460; DB 22; Length 277;  
Best Local Similarity 99.6%; Pred. No. 2.2e-147;

Matches 276; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENTENSVDKSKIKNLEPKIIHGESMDSGISLDSYKMDYPMGICITINNNKPHKSTG 60  
DB 1 MENTENSVDKSKIKNLEPKIIHGESMDSGISLDSYKMDYPMGICITINNNKPHKSTG 60  
QY 61 MTSRSGTDVDAANLRETFRNLYKEVRNKNLDTREIYELMDVSKEDSKRSSFCVYLLS 120  
DB 61 MTSRSGTDVDAANLRETFRNLYKEVRNKNLDTREIYELMDVSKEDSKRSSFCVYLLS 120  
QY 121 HGEGBIIFGTNGPVDLKKTINFFRGDRCSLTGPKFLIIQACRGTELDGCIETDSGVD 180  
DB 121 HGEGBIIFGTNGPVDLKKTINFFRGDRCSLTGPKFLIIQACRGTELDGCIETDSGVD 180  
QY 181 DMACHIPVEADFLYASTAGYYSWRNSKDSGWFISLCLAMLYADKLEFMHILTRVN 240  
DB 181 DMACHIPVEADFLYASTAGYYSWRNSKDSGWFISLCLAMLYADKLEFMHILTRVN 240  
QY 241 RKVATEFESEFSDATPHAKKOIPCIYVSMLEKELYFYH 277  
DB 241 RKVATEFESEFSDATPHAKKOIPCIYVSMLEKELYFYH 277

RESULT 9

ABJ01218  
ID ABJ01218 standard; Protein; 277 AA.  
XX

AC ABJ01218;

DT 18-SEP-2002 (first entry)

DE Human caspase-3 SEQ ID NO:12.

KW Human; caspase; rev-caspase; gene therapy; protease; apoptosis;  
KW cancer; autoimmune disease; cytostatic; immunosuppressive.

XX Homo sapiens.

XX US6376226-B1.

PD 23-APR-2002.

PF 26-APR-2000; 2000US-0561756.

PR 09-JAN-1998; 98US-070897P.

PR 08-JAN-1999; 99US-0227721.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Alnemri ES;

XX WPI; 2002-451275/48.

DR N-PSDB; ABT03966.

PT New rev-caspases engineered to contain the small subunit fused in frame  
PT N-terminal to the large subunit, which is in reverse order to the wild  
PT type caspases, are useful to treat cancer and autoimmune diseases  
XX

PS Disclosure; Fig 13; 81pp; English.

CC The present invention provides the protein and coding sequences of human  
CC rev-caspase-3, uncleavable rev-caspase-3 and rev-caspase-6. The sequences  
CC can be used in the gene therapy of cancer and autoimmune diseases. The  
CC present sequence is a protein described in the exemplification of the  
CC invention.  
XX

SQ Sequence 277 AA;

Query Match 99.8%; Score 1460; DB 23; Length 277;  
Best Local Similarity 99.6%; Pred. No. 2.2e-147;

Matches 276; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENTENSVDKSKIKNLEPKIIHGESMDSGISLDSYKMDYPMGICITINNNKPHKSTG 60  
DB 1 MENTENSVDKSKIKNLEPKIIHGESMDSGISLDSYKMDYPMGICITINNNKPHKSTG 60  
QY 61 MTSRSGTDVDAANLRETFRNLYKEVRNKNLDTREIYELMDVSKEDSKRSSFCVYLLS 120  
DB 61 MTSRSGTDVDAANLRETFRNLYKEVRNKNLDTREIYELMDVSKEDSKRSSFCVYLLS 120  
QY 121 HGEGBIIFGTNGPVDLKKTINFFRGDRCSLTGPKFLIIQACRGTELDGCIETDSGVD 180  
DB 121 HGEGBIIFGTNGPVDLKKTINFFRGDRCSLTGPKFLIIQACRGTELDGCIETDSGVD 180  
QY 181 DMACHIPVEADFLYASTAGYYSWRNSKDSGWFISLCLAMLYADKLEFMHILTRVN 240  
DB 181 DMACHIPVEADFLYASTAGYYSWRNSKDSGWFISLCLAMLYADKLEFMHILTRVN 240  
QY 241 RKVATEFESEFSDATPHAKKOIPCIYVSMLEKELYFYH 277  
DB 241 RKVATEFESEFSDATPHAKKOIPCIYVSMLEKELYFYH 277

RESULT 10  
AAN48945  
ID AAN48945 standard; Protein; 277 AA.  
XX



CC using mutated proteases and phosphatases whereby the catalytic cysteine  
CC residue of the enzymes are replaced with a serine or alanine residue to  
CC correct the problem of interference in SPA from extraneous oxidizing and  
CC alkylating agents. The mutation affects the catalytic properties of the  
CC enzyme but does not affect their binding properties. The invention  
CC claims for new ligands for use in SPA which have increased binding  
CC affinity for a tyrosine phosphatase or cysteine protease. The ligands  
CC contain at least two 4-phosphono(difluoromethyl) phenylalanine groups  
CC which increase binding affinity of the ligand to its respective enzyme.  
CC The assay can be used to determine the ability of new ligands and  
CC compound mixtures to competitively bind with an enzyme. The method is  
CC claimed to allow a better usage of SPA in the discovery of compounds for  
CC the treatment and study of diseases, e.g. diabetes, cancer and  
CC osteoporosis.

CC Sequence 277 AA:

Query Match 99.3%; Score 1453; DB 19; Length 277;  
Best Local Similarity 99.6%; Pred. No. 1.2e-146;  
Matches 276; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MENTENSVDKSKIKNEPKIHHGSEMDGSLDNSYKMDYPMGICITINNKNFKSTG 60  
DB 1 MENTENSVDKSKIKNEPKIHHGSEMDGSLDNSYKMDYPMGICITINNKNFKSTG 60  
QY 61 MTSRSGTDVDAANLRETFRNLYEVNKNKDLTREFEIVELMDVSKEDHSKRSSFVCLLS 120  
DB 61 MTSRSGTDVDAANLRETFRNLYEVNKNKDLTREFEIVELMDVSKEDHSKRSSFVCLLS 120  
QY 121 HEEEGIFETNGPVDLKTTNFRGDRCSLGTGPKLFTIIQACRGTELDGCIETDSGVD 180  
DB 121 HEEEGIFETNGPVDLKTTNFRGDRCSLGTGPKLFTIIQACRGTELDGCIETDSGVD 180  
QY 181 DMACHKIPVEADFLYASTAPGYYSWRNSKDSGSMFTOSLCAMKQYADKLEFMHILTRVN 240  
DB 181 DMACHKIPVEADFLYASTAPGYYSWRNSKDSGSMFTOSLCAMKQYADKLEFMHILTRVN 240  
QY 241 RKVATEFESEFSDATFHAHKKQIPCIYSMLTKELYFYH 277  
DB 241 RKVATEFESEFSDATFHAHKKQIPCIYSMLTKELYFYH 277

RESULT 12

AAB26763 standard; protein; 249 AA.

AC AAB26763;

DT 16-JAN-2001 (first entry)

DE Human caspase-1 protein sequence.

KW Apoptosis; detection; Nrf2; drug identification; prevention; treatment;

KW caspase; cancer; human.

OS Homo sapiens.

PN JP2000217598-A.

PD 08-AUG-2000.

PF 29-JAN-1999; 99JP-0022356.

PR 29-JAN-1999; 99JP-0022356.

PA (SUMO ) SUMITOMO CHEM CO LTD.

WIPI: 2000-605051/58.

PT Judgement of apoptosis-controlling activity for selecting drugs which  
DR can be used for preventing and treating various diseases caused by  
PT abnormality in apoptosis control -

PS Claim 5; Page 13; 17pp; Japanese.

CC A method for identifying drugs which exhibit apoptosis-controlling  
CC activity involves the use of a human Nrf2 protein. Nrf2 is a caspase  
CC substrate. The method involves detecting cleavage of the Nrf2 protein by  
CC caspase in the presence of a candidate drug. Detection of cleavage of the  
CC Nrf2 protein by caspase in the presence of a candidate drug indicates  
CC apoptosis inducing activity. The method can be used for selecting a drug  
CC which can be used for the prevention and the treatment of various  
CC diseases caused by abnormality in apoptosis control, such as cancer. The  
CC present sequence represents the human caspase-1 protein used in the  
CC method.

CC Sequence 249 AA:

Query Match 90.4%; Score 1322; DB 21; Length 249;  
Best Local Similarity 100.0%; Pred. No. 1.1e-132;  
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 SGISLDNSYKMDYPMGICITINNKNFKSTGMSRSGTDVDAANLRETFRNLYEVNKN 88  
DB 1 SGISLDNSYKMDYPMGICITINNKNFKSTGMSRSGTDVDAANLRETFRNLYEVNKN 88  
QY 89 NDLTREFEIVELMDVSKEDHSKRSSFVCLLSHGEEGIFETNGPVDLKTTNFRGDRG 148  
DB 89 NDLTREFEIVELMDVSKEDHSKRSSFVCLLSHGEEGIFETNGPVDLKTTNFRGDRG 148  
QY 149 RSLTGKPKLFTIIQACRGTELDGCIETDSGVDMDACHKIPVEADFLYASTAPGYYSWRN 208  
DB 149 RSLTGKPKLFTIIQACRGTELDGCIETDSGVDMDACHKIPVEADFLYASTAPGYYSWRN 208  
QY 121 RSLTGKPKLFTIIQACRGTELDGCIETDSGVDMDACHKIPVEADFLYASTAPGYYSWRN 180  
DB 121 RSLTGKPKLFTIIQACRGTELDGCIETDSGVDMDACHKIPVEADFLYASTAPGYYSWRN 180  
QY 209 SKDGSMTFOSLCAMKQYADKLEFMHILTRVNRKVAEFESFSDATFHAHKKQIPCIYSM 268  
DB 181 SKDGSMTFOSLCAMKQYADKLEFMHILTRVNRKVAEFESFSDATFHAHKKQIPCIYSM 240  
QY 269 LTKELYFYH 277  
DB 241 LTKELYFYH 249

RESULT 13

AAM47089 standard; protein; 277 AA.

AC AAM47089;

DT 20-JUL-1998 (first entry)

DE Rat interleukin-1 beta converting enzyme-related protease.

KW Interleukin-1 beta converting enzyme related protease;

KW ICE related protease; rat; apoptosis; inhibitor; brain ischaemia;

KW Alzheimer's disease; amyotrophic lateral sclerosis; head trauma;

KW neurodegenerative disorder.

OS Rattus sp.

PN WO9803642-A1.

PD 29-JAN-1998.

PF 15-JUL-1997; 97WO-US10999.

PR 22-JUL-1996; 96US-0022049.

PA (ELIL ) LILLY & CO ELI.

PI Ni B. Paul SM. Wu X.

WIPI: 1998-120767/11.

DR N-PSDB; AAV13959.

PT Rat interleukin-1 beta converting enzyme related protease - used for

PT treating Alzheimer's disease, amyotrophic lateral sclerosis, and  
 PT other neurodegenerative disorders  
 PS Claim 1; Page 65; 76pp; English.  
 XX  
 CC This polypeptide comprises a novel rat interleukin-1 beta  
 CC converting enzyme (ICE) related protease, overexpression of which  
 CC may be involved in a neuronal death cascade. The amino acid  
 CC sequence was deduced from a cDNA clone (see AAV1959) isolated from a  
 CC rat brain cDNA library. ICE related protease is present in the  
 CC central nervous system and is enriched in central neurons  
 CC including pyramidal neurons and granule neurons of the hippocampus  
 CC and cerebral cortex. An expression vector capable of producing the  
 CC ICE related protease in a host cell is claimed. The protease can  
 CC be used in a claimed method to identify compounds that inhibit  
 CC apoptosis. Such inhibitors can be used to treat Alzheimer's  
 CC disease, amyotrophic lateral sclerosis (ALS), head trauma or other  
 CC neurodegenerative disorders in humans (all claimed). Antibodies  
 CC raised against the protease may be used for diagnosis of these  
 CC disease states, or in their treatment.  
 CC  
 SQ Sequence 277 AA;  
 XX  
 Query Match 89.1%; Score 1304; DB 19; Length 277;  
 Best Local Similarity 88.4%; Pred. No. 1e-130; Indels 0; Gaps 0;  
 Matches 245; Conservative 13; Mismatches 19;  
 QY 1 MENTENSVDSSKIKLEPKIIGHSESDSGISLDNSYKMDYEMGLCIIINKNFHKSTG 60  
 DB 1 MONTNRTSVDSKSIINFEKTIHSGSKMSDGIYDSYKMDYEMGLCIIINKNFHKSTG 60  
 QY 61 MTSRSGTVDAAANLRETFRNKLYEVRNKNNDLTREIIVELMRDVSKEHRSKRSFVCVLLS 120  
 DB 61 MSRRNSTDVDAANLRETFRNKLYEVRNKNNDLTREIIVELMRDVSKEHRSKRSFVCVLLS 120  
 QY 121 HGEBSGIIFGTNGPVDLKKTINFEFGDRCRSLTGKPKLFIQACRGTELDGCIETDSTGTD 180  
 DB 121 HGEBSGIIFGTNGPVDLKKTINFEFGDRCRSLTGKPKLFIQACRGTELDGCIETDSTGTD 180  
 QY 181 DMACHKIPVEADFLYASTAGYYSWRNSKDSWFIQSLCAALKQYADKLEFMHILTRVN 240  
 DB 181 DMACHKIPVEADFLYASTAGYYSWRNSKDSWFIQSLCAALKQYADKLEFMHILTRVN 240  
 QY 241 RKVATFEFSFSDATFHAKKQIPCIIVSMLTKELYFYH 277  
 DB 241 RKVATFEFSFSDATFHAKKQIPCIIVSMLTKELYFYH 277  
 XX  
 RESULT 14  
 AAG78712  
 ID AAG78712 standard; Protein; 277 AA.  
 XX  
 AC AAG78712;  
 XX  
 DT 11-DEC-2001. (first entry)  
 XX  
 DE Pig caspase #2.  
 XX  
 KW Pig; caspase; inflammation; infection.  
 XX  
 OS Sus scrofa.  
 XX  
 PN JP2001169785-A.  
 XX  
 PD 26-JUN-2001.  
 XX  
 PE 03-OCT-2000; 2000JP-0303931.  
 XX  
 PR 05-OCT-1999; 99JP-0284829.  
 XX  
 PA (NORO) NORINSUISANSO KACHIKU EISEI.  
 PA (MUNE/) MUNETA Y.  
 PA (MORI/) MORI Y.

PA (SHIM/) SHIMOCHI Y.  
 PA (ARAI/) ARAI K.  
 XX  
 DR WPI; 2001-592539/67.  
 DR N-PSDB; AAI66510.  
 XX  
 PT Structural gene of swine caspase family, used for artificial control of  
 PT inflammatory reactions in infectious diseases  
 PS Claim 6; Page 16; 23pp; Japanese.  
 XX  
 CC The present invention provides two versions of a porcine caspase protein.  
 CC These can be used to control inflammatory reactions to microbial or viral  
 CC infectious diseases. The present sequence is one version of the protein  
 CC of the invention.  
 CC  
 SQ Sequence 277 AA;  
 XX  
 Query Match 88.6%; Score 1296; DB 22; Length 277;  
 Best Local Similarity 88.4%; Pred. No. 7.5e-130; Indels 0; Gaps 0;  
 Matches 245; Conservative 11; Mismatches 21;  
 QY 1 MENTENSVDSSKIKLEPKIIGHSESDSGISLDNSYKMDYEMGLCIIINKNFHKSTG 60  
 DB 1 MENTNRTSVDSKSIKLEPKIIGHSESDSGISLDNSYKMDYEMGLCIIINKNFHKSTG 60  
 QY 61 MTSRSGTVDAAANLRETFRNKLYEVRNKNNDLTREIIVELMRDVSKEHRSKRSFVCVLLS 120  
 DB 61 MACNSGTVDAAANLRETFRNKLYEVRNKNNDLTREIIVELMRDVSKEHRSKRSFVCVLLS 120  
 QY 121 HGEBSGIIFGTNGPVDLKKTINFEFGDRCRSLTGKPKLFIQACRGTELDGCIETDSTGTD 180  
 DB 121 HGEBSGIIFGTNGPVDLKKTINFEFGDRCRSLTGKPKLFIQACRGTELDGCIETDSTGTD 180  
 QY 181 DMACHKIPVEADFLYASTAGYYSWRNSKDSWFIQSLCAALKQYADKLEFMHILTRVN 240  
 DB 181 DMACHKIPVEADFLYASTAGYYSWRNSKDSWFIQSLCAALKQYADKLEFMHILTRVN 240  
 QY 241 RKVATFEFSFSDATFHAKKQIPCIIVSMLTKELYFYH 277  
 DB 241 RKVATFEFSFSDATFHAKKQIPCIIVSMLTKELYFYH 277  
 XX  
 RESULT 15  
 AAU05395  
 ID AAU05395 standard; Protein; 277 AA.  
 XX  
 AC AAU05395;  
 XX  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE Mouse caspase 3.  
 XX  
 KW Mouse; caspase 3; apoptosis; hyperproliferative disorder; hepatitis;  
 KW viral infection; haematopoietic disorder; autoimmune disorder;  
 KW atherosclerosis; neurological disorder.  
 XX  
 OS Mus musculus.  
 XX  
 PN W020015310-A1.  
 XX  
 PD 26-JUL-2001.  
 XX  
 PE 11-JAN-2001; 2001WO-US00888.  
 XX  
 PR 18-JAN-2000; 2000US-0484617.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 PA Zhang H, Cowsett LM;  
 PI WPI; 2001-442252/47.  
 XX  
 DR N-PSDB; AAS10510.

XX New antisense compound to inhibit caspase 3 is useful for treating  
PT hepatitis and atherosclerosis -  
XX  
PS Disclosure; Page 96-97; 127pp; English.  
XX

CC The present sequence representing mouse caspase 3 is described  
CC in an invention relating to novel antisense oligonucleotides  
CC (AS10517-AS10676) and methods of using these compounds for the  
CC modulation of caspase 3 expression. The caspase 3 antisense  
CC oligonucleotides specifically hybridise with and inhibit the  
CC expression of caspase 3. Antisense compounds targeted to caspase 3  
CC are useful to inhibit caspase 3 expression in cells or tissues and  
CC to modulate apoptosis. The caspase 3 antisense oligonucleotides are  
CC useful for treating disorders associated with expression of caspase 3.  
CC Such disorders include hyperproliferative disorders (e.g. cancer),  
CC viral infections (e.g. hepatitis), haematopoietic disorders, autoimmune  
CC disorders, atherosclerosis and neurological disorders (e.g. Alzheimer's  
CC disease).  
XX

SQ Sequence 277 AA:

Query Match 88.4%; Score 1293; DB 22; Length 277;  
Best Local Similarity 86.6%; Pred. No. 1.6e-129;  
Matches 240; Conservative 20; Mismatches 17; Indels 0; Gaps 0;

OY 1 MENTENSVDKSIKNEPKIHGSESDSGISLDNSYKMDYPMGICITINNNKPHKSTG 60  
DB 1 MNNNTSVDSKSIINNFVKTIGSKSVDSGITYDSSYKMDYPMGICITINNNKPHKSTG 60  
OY 61 MTSRSGTDVDAANLRETFRNLYEVNRKNDLTREIYELMDVSKEDHSKRSSFVCVLLS 120  
DB 61 MSSRSGTDVDAANLRETFRNLYEVNRKNDLTREIYELMDVSKEDHSKRSSFVCVLLS 120  
OY 121 HGEELIIRCTNGPVDLKRTTNFRGDRCSLTGKPKLFTIOACRGTELDGCIETDSGVD 180  
DB 121 HGEELIIRCTNGPVDLKRTTNFRGDRCSLTGKPKLFTIOACRGTELDGCIETDSGVD 180  
OY 181 DWACHKIPVADFLYAVSTAPGYYSWRNSKDSGSMFTOSLCAMLKQYADKLEFMHILTRVN 240  
DB 181 EMACKRIPEADFLYAVSTAPGYYSWRNSKDSGSMFTOSLCAMLKQYADKLEFMHILTRVN 240  
OY 241 RRVATEFESFSDATFNAKQIPICIYSMLTKELYFYH 277  
DB 241 RRVATEFESFSDATFNAKQIPICIYSMLTKELYFYH 277

Search completed: December 2, 2002, 12:56:04  
Job time : 32.0431 secs

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OM protein - protein search, using sw model

Run on: December 2, 2002, 12:54:49 ; Search time 26.2672 Seconds  
(Without alignments)  
2172.860 Million cell updates/sec

Title: US-09-895-263-4  
Perfect score: 1463  
Sequence: 1 MENTENSVDSKSIKNLEPKI.....AKQIPCIYSMLTKELYFH 277

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SEPREMBL\_21:\*  
1: sp-archaea:\*  
2: sp-bacteria:\*  
3: sp-fungi:\*  
4: sp-human:\*  
5: sp-invertebrate:\*  
6: sp-mammal:\*  
7: sp-mhc:\*  
8: sp-organelle:\*  
9: sp-phage:\*  
10: sp-plant:\*  
11: sp-rodent:\*  
12: sp-virus:\*  
13: sp-vertebrate:\*  
14: sp-unclassified:\*  
15: sp-virus:\*  
16: sp-bacteriap:\*  
17: sp-archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1463	100.0	277	4	Q96ANI
2	1441	98.5	277	4	Q96ANI
3	1296	88.6	277	6	Q96KRP2
4	1040	71.1	220	11	Q95NDS
5	958	65.5	283	13	Q93417
6	854	58.4	182	6	Q93417
7	782	53.5	282	13	Q98U18
8	761	52.0	318	13	Q91B65
9	745	50.9	303	11	Q98550
10	526	36.0	276	11	Q99M47
11	525.5	35.9	293	4	Q98QF7
12	525.5	35.9	302	13	Q91B69
13	524	35.8	303	13	Q91B66
14	516	35.3	276	11	Q9D089
15	515	35.2	304	13	Q93415
16	503.5	34.4	277	11	Q93397

17	484	33.1	326	5	Q9GV88	Q9GV88 hydra atten
18	437.5	29.9	482	11	Q9JHX4	Q9JHX4 rattus norv
19	436	29.8	454	11	Q9ROT0	Q9ROT0 mus musculu
20	435	29.7	480	11	Q9J110	Q9J110 m caspase 8
21	434	29.7	454	11	Q9JHK1	Q9JHK1 rattus norv
22	432.5	29.6	482	13	Q90WU1	Q90WU1 gallus gall
23	431.5	29.5	131	11	Q9CXM4	Q9CXM4 mus musculu
24	423	28.9	399	13	Q91B63	Q91B63 xenopus lae
25	422.5	28.9	476	13	Q91B3	Q91B3 brachydanto
26	422	28.8	308	5	Q9NHE9	Q9NHE9 drosophila
27	422	28.8	308	5	Q9VER9	Q9VER9 drosophila
28	421	28.8	456	4	Q9COK4	Q9COK4 homo sapien
29	421	28.8	538	4	Q9TD15	Q9TD15 homo sapien
30	417	28.5	416	4	Q9B062	Q9B062 homo sapien
31	404	27.6	403	13	Q90WU0	Q90WU0 gallus gall
32	383.5	26.2	500	13	Q91B64	Q91B64 xenopus lae
33	374.5	25.6	520	13	Q91B62	Q91B62 xenopus lae
34	360	24.6	417	5	Q9Y106	Q9Y106 pristionchu
35	349	23.9	479	4	Q8WY08	Q8WY08 homo sapien
36	328.5	22.5	435	4	Q9BUP7	Q9BUP7 homo sapien
37	327.5	22.4	452	11	Q95194	Q95194 rattus norv
38	325	22.2	353	11	Q9R0S9	Q9R0S9 mus musculu
39	324	22.1	423	13	Q91B67	Q91B67 xenopus lae
40	310.5	21.2	268	5	Q9TZP6	Q9TZP6 caenorhabdi
41	310.5	21.2	536	5	Q18203	Q18203 caenorhabdi
42	306.5	21.0	263	5	Q9TGP5	Q9TGP5 caenorhabdi
43	306.5	21.0	826	5	Q91055	Q91055 caenorhabdi
44	302.5	20.7	347	5	Q9GV89	Q9GV89 hydra atten
45	283	19.3	383	11	Q99M88	Q99M88 rattus norv

#### ALIGNMENTS

RESULT 1	ID	Q96ANI	PRELIMINARY:	PRT:	277 AA.
AC	Q96ANI				
DT	01-DEC-2001 (TREMBLrel. 19, Created)				
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)				
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)				
DE	Hypothetical 31.6 kDa protein.				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=LYMPH;				
RA	Strausberg R.;				
RL	Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL: BC016926; AAH16926.1; -				
DR	InterPro: IPR002398; ICE.				
DR	InterPro: IPR002138; ICE.				
DR	InterPro: IPR001309; ICE_P20.				
DR	Pfam: PF00655; ICE_P10; 1.				
DR	Pfam: PF00656; ICE_P20; 1.				
DR	PRINTS: PR00376; ILICENZYME.				
DR	PROSITE: PS01122; CASPASE_CYS; UNKNOWN_1.				
DR	PROSITE: PS01121; CASPASE_HIS; UNKNOWN_1.				
DR	PROSITE: PS0207; CASPASE_P10; 1.				
DR	PROSITE: PS0208; CASPASE_P20; 1.				
KW	Hypothetical protein.				
SQ	SEQUENCE 277 AA; 31608 MW; 2F35CD3BCF7F64A CRC64;				
Query Match	100.0%;	Score 1463;	DB 4;	Length 277;	
Best Local Similarity	100.0%;	Pred. No. 1.6e-114;			
Matches 277;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
OY	1 MENTENSVDSKSIKNLEPKIHGSEMSDGSISLDNSYKMDYPENGGLCIITNNKHFHSTG 60				
DB	1 MENTENSVDSKSIKNLEPKIHGSEMSDGSISLDNSYKMDYPENGGLCIITNNKHFHSTG 60				

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Qy 61 MTSRSGTDVDAANLRETFRNLTKEVRNKNNDLTREIIVELMRDYSKEDHSKRSSFVCYLLS 120
Db 61 MTSRSGTDVDAANLRETFRNLTKEVRNKNNDLTREIIVELMRDYSKEDHSKRSSFVCYLLS 120
Qy 121 HGEGLIIFGTNGVVDLKKITNFRGDRCSLTGKPKLFIIOACRGTELDGCIETDSGVD 180
Db 121 HGEGLIIFGTNGVVDLKKITNFRGDRCSLTGKPKLFIIOACRGTELDGCIETDSGVD 180
Qy 181 DMACHKIPVEADFLYASTAGYYSWRNSKDGSMFIOSLCAMLKQYADKLEFMHILTRVN 240
Db 181 DMACHKIPVEADFLYASTAGYYSWRNSKDGSMFIOSLCAMLKQYADKLEFMHILTRVN 240
Qy 241 RKVATEFESEFSFDTAFHAKKOIPICVSMLTKELYFYH 277
Db 241 RKVATEFESEFSFDTAFHAKKOIPICVSMLTKELYFYH 277

RESULT 2
Q96KP2 PRELIMINARY: PRT: 277 AA.
AC 096KP2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Caspase-3.
GN CASP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RA Vallette F.M.;
RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
RN 12
RP SEQUENCE FROM N.A.
RA Oliver L.J.;
RL "Control of the activation of the procaspase-3 by a sequence located
RT at the N-terminus of the p17 subunit."
RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ413269; CAC88866.1;
DR InterPro: IPR002398; ICE_p10.
DR InterPro: IPR002138; ICE_p10.
DR InterPro: IPR001309; ICE_p20.
DR Pfam: PF00655; ICE_p10; 1.
DR Pfam: PF00656; ICE_p20; 1.
DR PRINTS: PR00376; TLBCEZYME.
DR PROSITE: PS01122; CASPASE_CYS; UNKNOWN_1.
DR PROSITE: PS01121; CASPASE_HIS; UNKNOWN_1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
SO SEQUENCE 277 AA; 31642 MW; 6162767BD2DE021 CRC64;

Query Match 98.5%; Score 1441; DB 4; Length 277;
Best Local Similarity 98.2%; Pred. No. 1,1e-112;
Matches 272; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Qy 241 RKVATEFESEFSFDTAFHAKKOIPICVSMLTKELYFYH 277
Db 241 RKVATEFESEFSFDTAFHAKKOIPICVSMLTKELYFYH 277

RESULT 3
Q95ND5 PRELIMINARY: PRT: 277 AA.
AC 095ND5;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE Caspase-3.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OX NCBI_TaxID=9823;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE-21334413; PubMed-11440638;
RA Muneta Y., Shimojima Y., Mori Y.;
RT "Porcine caspase-3: cloning and its activity during apoptosis of
RT porcine PK15 cells induced by porcine Fas-ligand."
RL J. Interferon Cytokine Res. 21:409-415(2001).
DR EMBL: AB029345; BAB5544.1;
DR MEROPS: C14.003;
DR InterPro: IPR002138; ICE_p10.
DR InterPro: IPR001309; ICE_p10.
DR Pfam: PF00655; ICE_p10; 1.
DR Pfam: PF00656; ICE_p20; 1.
DR PROSITE: PS01122; CASPASE_CYS; UNKNOWN_1.
DR PROSITE: PS01121; CASPASE_HIS; UNKNOWN_1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
SO SEQUENCE 277 AA; 31379 MW; 616C0F56141B012B CRC64;

Query Match 88.6%; Score 1296; DB 6; Length 277;
Best Local Similarity 88.4%; Pred. No. 1,5e-100;
Matches 245; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

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Qy 1 MENTENSVDKSIKLEPKITIHGSEMSDGLSDYSKMDYEMGLCIITNNKFNHSTG 60
Db 1 MENTENSVDKSIKLEPKITIHGSEMSDGLSDYSKMDYEMGLCIITNNKFNHSTG 60
Qy 61 MTSRSGTDVDAANLRETFRNLTKEVRNKNNDLTREIIVELMRDYSKEDHSKRSSFVCYLLS 120
Db 61 MTSRSGTDVDAANLRETFRNLTKEVRNKNNDLTREIIVELMRDYSKEDHSKRSSFVCYLLS 120
Qy 121 HGEGLIIFGTNGVVDLKKITNFRGDRCSLTGKPKLFIIOACRGTELDGCIETDSGVD 180
Db 121 HGEGLIIFGTNGVVDLKKITNFRGDRCSLTGKPKLFIIOACRGTELDGCIETDSGVD 180
Qy 241 RKVATEFESEFSFDTAFHAKKOIPICVSMLTKELYFYH 277
Db 241 RKVATEFESEFSFDTAFHAKKOIPICVSMLTKELYFYH 277

RESULT 4
Q90W14 PRELIMINARY: PRT: 220 AA.
AC 090W14;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE CPB32 apoptotic protease (Fragment).
GN CASP3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Denis F., Alam A., Cohen L., Hartgers F., Braun M., Martinez O.,
RA Fortin J.-P., Sekaly R.-P.;
RT "Multiple Pathways of Apoptosis Converging on the CPP32 Protease.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63720; AAD09504.1; -
DR HSSP; P42574; IPAU.
DR MEROPS; C14.003; -
DR MGD; MGI:107739; Casp3.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR Pfam; PF00655; ICE_P10; 1.
DR Pfam; PF00656; ICE_P20; 1.
DR PRINTS; PR00376; ILIBCEZYME.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KM Protease.
FT NON_TER
SQ SEQUENCE 220 AA; 25050 MW; FE7F4857C4EBA544 CRC64;

Query Match 71.18; Score 1040; DB 11; Length 220;
Best Local Similarity 86.8%; Pred. No. 2.9e-79;
Matches 191; Conservative 18; Mismatches 11; Indels 0; Gaps 0;

QY 58 STGTSRGTVDVDAANRETFRNLKYEVRNKNNDLTREIYELMDVSKEDHSKRSFVCV 117
DB 1 STGMSRANGTDVDAANRETFRNLKYEVRNKNNDLTREIYELMDVSKEDHSKRSFVCV 60
QY 118 LLSHGEELIIFGTNGPVLDLKITNFRGDRCSLTGKPKLFTIOACRGTELDGCIETDSG 177
DB 61 ILSHGDEGVLYGTNGPVLELKLTSFRRGDRCSLTGKPKLFTIOACRGTELDGCIETDSG 120
QY 178 VDDDMACHTPVEADFLYATSTAPGYYSWRNSKDGSWFIOSLCAMLYADKLEFMHILT 237
DB 121 TDEMACQKTPVEADFLYATSTAPGYYSWRNSKDGSWFIOSLCAMLYADKLEFMHILT 180
QY 238 RVNRKYATEFESFSDATFPAKQIIPCIVSMLTKELYFYH 277
DB 181 RVNRKYATEFESFSDATFPAKQIIPCIVSMLTKELYFYH 220

RESULT 5
093417 PRELIMINARY; PRT; 283 AA.
AC 093417;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Caspase-3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Johnson A.L., Bridgman J.T.;
RT "Caspase-3 and -6 expression and enzyme activity in hen granulosa
RT cells.";
RL Biol. Reprod. 62:589-598(2000).
DR EMBL; AF083029; AAC32602.1; -
DR HSSP; P42574; IPAU.
DR MEROPS; C14.003; -
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
SQ SEQUENCE 182 AA; 20408 MW; B5860CC6596C21BE7 CRC64;
FT NON_TER
Query Match 58.4%; Score 854; DB 6; Length 182;
```

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DR Pfam; PF00655; ICE_P10; 1.
DR Pfam; PF00656; ICE_P20; 1.
DR PRINTS; PR00376; ILIBCEZYME.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 283 AA; 31675 MW; 161242DDEFD4DC4F CRC64;

Query Match 65.5%; Score 958; DB 13; Length 283;
Best Local Similarity 66.4%; Pred. No. 2.9e-72;
Matches 180; Conservative 43; Mismatches 46; Indels 2; Gaps 2;

QY 5 ENSVDSKSIKMLEPKRIHGSSESDSGISLDNSKYKMDPEMGLCTIINNNKPKSTGMSR 64
DB 13 EDVSDARSFPGSGMNLPAKSKVDSGLIPDDSYRDYDEIGVCYIINNNKPNFRDGLSSR 72
QY 65 SGTVDANLKEETFRNLKYEVRNKNNDLTREIYELMDVSKEDHSKRSFVCVLLSHGEE 124
DB 73 SGTVDADAASVREVEPKLGYKVLNNDLSRDLFKLKNVSEEDHSKRSFVCVLLSHGDE 132
QY 125 GIIFGTNGPVLDLKITNFRGDRCSLTGKPKLFTIOACRGTELDGCIETDSGVDPMAC 184
DB 133 GLIFGTDPLELKLUTSLFRGDKCSLTGKPKLFTIOACRGTELDGCIETDSG-PDEYVC 191
QY 185 HKIPEADFLYATSTAPGYYSWRNSKDGSWFIOSLCAMLYADKLEFMHILT RVNRKYA 244
DB 192 QKIPVEADFLYATSTAPGYYSWRNSKDGSWFIOSLCAMLYADKLEFMHILT RVNRKYA 251
QY 245 TEFESEFSDATFPAKQIIPCIVSMLTKELYFYH 275
DB 252 -EYESCSTRQDFENAKQIIPCIVSMLTKELYFYH 281

RESULT 6
077623 PRELIMINARY; PRT; 182 AA.
AC 077623;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Caspase-3 (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Rueda B.R., Hendry I.R., Tilly J.L., Hamernik D.L.;
RT "Accumulation of Caspase-3 mRNA and induction of Caspase Activity in
RT the Ovine Corpus Luteum Following Prostaglandin-F2a Treatment in
RT Vivo.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF068837; AAC25713.1; -
DR HSSP; P42574; IPAU.
DR MEROPS; C14.003; -
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR Pfam; PF00655; ICE_P10; 1.
DR Pfam; PF00656; ICE_P20; 1.
DR PRINTS; PR00376; ILIBCEZYME.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
FT NON_TER
SQ SEQUENCE 182 AA; 20408 MW; B5860CC6596C21BE7 CRC64;
FT NON_TER
Query Match 58.4%; Score 854; DB 6; Length 182;
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ID 088550 PRELIMINARY; PRT; 303 AA.
AC 088550;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Caspase-7.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Forghani F., Roy S.;
RT "Rat caspase-7 sequence."
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF072124; AAC24011.1;
DR HSSP: P42574; 1PAU.
DR MEROPS: C14.004; -.
DR InterPro: IPR002398; ICE.
DR InterPro: IPR002138; ICE_P10.
DR InterPro: IPR001309; ICE_P20.
DR Pfam: PF00655; ICE_P10; 1.
DR Pfam: PF00656; ICE_P20; 1.
DR PRINTS: PR00376; ILBCENZTME.
DR SMART: SM00115; CASc; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
SQ SEQUENCE 303 AA; 34324 MW; A71728754BF199DD CRC64;

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Query Match
Best Local Similarity 53.9%; Score 745; DB 11; Length 303;
Matches 153; Conservative 41; Mismatches 79; Indels 12; Gaps 3;

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QY 3 NTESVVSQS-----INKLEPKIIHGSESDSGISLDN---SYKMDYPMGLCIITNNK 53
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 17 STEDGVDAKPRSTLTSSILWKKKNAKMCVSTTRDVRVLYLMDPEKMKKCIITNNK 76
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 77 NFDKATMDVNRGTDGKDEALFKCFRSLGFEVYVNDSCAKMODLLRRASEEDHSNSAC 136
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 114 FVCVLLSHGEGIIFTNGPVDLKKITNFFRGDRCSLTGPKLIIOACRGTEDCGIE 173
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 137 FACVLLSHGEGNLTGKDGVPKIDLTNHFSGDKLTLEPKLFTIOACRGTEDDGIQ 196
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 174 TDSGVDDMAC--HKIPVEADFLYASTAGYYSWRNSKDGSMFQISICAMLKQYADKL 230
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 197 ADSGPIINDTDANPKYKIPVEADFLFAYSTVPGYYSWRNPKGSMFVQALCSTLNEHGKDL 256
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 231 EFMIILTRVNRKVAETEFSEFSDATFAKKKQIPCVSKLTLELYP 275
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 257 EIMQILTRVNDVARHFEQSDDPRFNEKKQIPCMVSMLTRELYP 301
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 10
099M47 PRELIMINARY; PRT; 276 AA.
AC 099M47;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Caspase 6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;

```

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RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC002022; AAH02022.1; -.
DR HSSP: P42574; 1PAU.
DR MGD: MGI:1312921; Casp6.
DR InterPro: IPR002398; ICE.
DR InterPro: IPR002138; ICE_P10.
DR InterPro: IPR001309; ICE_P20.
DR Pfam: PF00655; ICE_P10; 1.
DR Pfam: PF00656; ICE_P20; 1.
DR PRINTS: PR00376; ILBCENZTME.
DR SMART: SM00115; CASc; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
SQ SEQUENCE 276 AA; 31563 MW; 5965C5932A127B6C CRC64;

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Query Match
Best Local Similarity 36.0%; Score 526; DB 11; Length 276;
Matches 104; Conservative 42; Mismatches 93; Indels 12; Gaps 1;

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QY 37 YKMDYPMGLCIITNNKFNKSTGMRSGTVDVDAANLRETFRNLYEVRNKNNDLREEL 96
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 20 YKMDKRGVALLFNHERFWHLTLPERKGTNADRNLTFRSSDLGFEVKCFNDLAEEL 79
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 97 VELARDVSKEDHSKRSSFEVCLVLSHGEGLIFGTNGPVDLKKITNFFRGDRCSLTGPKR 156
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 80 LKIHVEVTSIIHDAADFCEVFLSHGEGNHVYAYDAKIEIQTLTGKFDKQCSLVGKKR 139
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 157 LFIQACRGTEDCGIETDSGVD-----DDMACHKIPVEADFLYASTAGY 204
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 140 IFIIQACRGSQHDVFPVPLDVVDHOTDKLDNTQYVDAASVYTLPAQADFLMCYSVAEGY 199
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 205 SWRNSKDGSMFQISICAMLKQYADKLEFMHILTRVNRKVAETEFSEFSDATFAKKQIQ 264
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 200 SHRETVNSWYTDLCCEMLARAGSSLEFTELLTVNRKVSQRVRVCKPDAGIKGQVPC 259
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 265 IYSMLTKELYP 275
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 260 FASMLTKLHF 270
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

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RESULT 11
09BOE7 PRELIMINARY; PRT; 293 AA.
AC 09BOE7;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Caspase 6; apoptosis-related cysteine protease.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC004460; AAH04460.1; -.
DR EMBL: BC000305; AAH00305.1; -.
DR HSSP: P42574; 1PAU.
DR MEROPS: C14.005; -.
DR InterPro: IPR002398; ICE.
DR InterPro: IPR002138; ICE_P10.
DR InterPro: IPR001309; ICE_P20.
DR Pfam: PF00655; ICE_P10; 1.
DR Pfam: PF00656; ICE_P20; 1.

```

```
DR PRINTS: PR00376; ILIBCENZYM.
DR SMART; SM00115; CASc. 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR Protease.
SQ SEQUENCE 293 AA; 33310 MW; 0738AE4F9791EBD7 CRC64;

Query Match 35.9%; Score 525.5; DB 4; Length 293;
Best Local Similarity 41.5%; Pred. No. 4,5e-36;
Matches 105; Conservative 42; Mismatches 93; Indels 13; Gaps 1;

QY 37 YKMDYPEMGLCIITNNKHFHSTGTSRSGTDVDAANLRETFRNLYKEVNRKNDLREEL 96
DB 37 YKMDHRRRCIALIFNHRERFWMLTLPERGTCTCDNRDLRRESDLFEFKCFNDLAEEL 96
QY 97 VELMDVSKEDSKSSKSSFCVLLSHGEGIIIFGTNGPVDLKKITNFFGRDRCSLTGKPK 156
DB 97 LKRIHEVSVSHADADCFVCFVLSHGEGNHIIAYDAKIEIQLTLGLFKGDKCHSLVGKPK 156
QY 157 LFIIOACRGTELDGCI-----ETDSGVDDMACHKIPVADFLVYSTAPGY 203
DB 157 LFIIOACRGNDHVPYIPLDVVDNQTETKLDITNTEVDASVYTLPGADGFLMKCYVAEGY 216
QY 204 YSMRNSKDSNFIQSLCAMLKQYADKLEFPMHILTRVNRKVAATEFESEFSDATFHAKKOIP 263
DB 217 YSHRETVNSWYIODLCENLKGKYSLEFTELLTLVNRKVSQRARDVFCQKPSAIGKKQVP 276
QY 264 CIVSMLTKELYFY 276
DB 277 CFASMLTKKLHFF 289

RESULT 12
ID 0918S9 PRELIMINARY; PRT; 302 AA.
AC 0918S9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Caspase 6.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Laing K.J., Holland J., Bonilla S., Cunningham C., Secombes C.J.;
RT "Cloning and sequencing of caspase 6 in rainbow trout, Oncorhynchus
RT mykiss, and analysis of its expression under conditions known to
RT induce apoptosis.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF212219; AAF73848.1; -.
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.005; -.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR Pfam; PF00655; ICE_P10; 1.
DR Pfam; PF00656; ICE_P20; 1.
DR PRINTS; PR00376; ILIBCENZYM.
DR SMART; SM00115; CASc. 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 302 AA; 34082 MW; 5A6BSF28A0CFA660 CRC64;

Query Match 35.9%; Score 525.5; DB 13; Length 302;
Best Local Similarity 36.8%; Pred. No. 4,7e-36;
Matches 109; Conservative 63; Mismatches 97; Indels 27; Gaps 5;
```

```
QY 2 ENTENSV--DSKSTKNLEPKIIHSESM-----DSGISLD--NSYKMDYPEMGLCIIT 49
DB 7 KDTKGSLEKKNKTSQTGP-----SEMLTETDGYFCSSSFSDPAEYKKNHKKRRGIALI 61
QY 50 INNKNFHKSTGTSRSGTDVDAANLRETFRNLYKEVNRKNDLREELVELMDRVSKEDHS 109
DB 62 FNEHFHWMHLMRPNRNTNDRSLNLYKRFEDLNFEVAFNLKAEVLDIOISCAEAENHA 121
QY 110 KRSEFVCLLSHGEIIIFGTNGPVDLKKITNFFGRDRCSLTGKPKLFIIOACRGTE-- 167
DB 122 DADCFVCFVLSHGEGNHVYAYDDKIALIODITALEFKGDKCSLVGKPKLFIIOACRGKHD 181
QY 168 -----LDCGIEFDSGVDDMACHKIPVADFLVYSTAPGYYSMRNSKDSGSWFIQSL 219
DB 182 DPVTPMDVYDEVKTEVNVDAAGVYTLPGADGFLMKCYVAEGYSHRETIINGSWYIIDL 241
QY 220 CAMLKQYADKLEFPMHILTRVNRKVAATEFESEFSDATFHAKKOIPCIYSMLTKELYF 275
DB 242 CGAMRKFQDSLEFTELLTLVNRKVSMSRGVNCNDKTAIGKKQVPCFASMLTKLYF 297

RESULT 13
ID 091B66 PRELIMINARY; PRT; 303 AA.
AC 091B66;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Caspase-6.
GN XCASPASE-6.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-20209426; PubMed-10744739;
RA Nakajima K., Takahashi A., Yaoita Y.;
RT "Structure, expression and function of the Xenopus laevis caspase
RT family ";
RL J. Biol. Chem. 275:10484-10491(2000).
DR EMBL; AB038169; BAA94747.1; -.
DR HSSP; P42574; 1CP3.
DR MEROPS; C14.005; -.
DR InterPro; IPR002398; ICE.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR Pfam; PF00655; ICE_P10; 1.
DR Pfam; PF00656; ICE_P20; 1.
DR PRINTS; PR00376; ILIBCENZYM.
DR SMART; SM00115; CASc. 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 303 AA; 34132 MW; 4C54A0A607C69756 CRC64;

Query Match 35.8%; Score 524; DB 13; Length 303;
Best Local Similarity 42.4%; Pred. No. 6,3e-36;
Matches 109; Conservative 48; Mismatches 86; Indels 14; Gaps 4;

QY 31 ISLDS--YKMDYPEMGLCIITNNKHFHSTGTSRSGTDVDAANLRETFRNLYKEVRNK 86
DB 42 VLDLSAEYIMHKKRGALILNHNEDFYQLKGSFRGNTSMNLRLITLDGFGVQNY 101
QY 89 NDLREELVELMDRVSKEDSKSSKSSFCVLLSHGEGIIIFGTNGPVDLKKITNFFGRDR 148
DB 102 YNLRTMDVLEKIQEASTDHSNADCFVLSHGEGKHIIYSYDSLIDQELTNPFKGDGC 161
QY 149 RSLTKPKLFIIOACRGTELDGCI-----ETDS-----GVDDMACHKIPVADFLVAY 197
DB 149 RSLTKPKLFIIOACRGTELDGCI-----ETDS-----GVDDMACHKIPVADFLVAY 197
```

Db 162 KSLVGRKPIILQACRGEKHDEPLPKDEVSYELTNTEYDASLC-TLPAGADFLMICY 220  
 QY 198 STAPGYYSWNSNDGSGFIQSLCAMLKQYADKLEFPHILTRVNRKVAITEEFSFDPATFH 257  
 Db 221 SVAEGYSHRETVNGSVYIDLCVAVKAVASLEFTEILLVNRKVSORSVEYCNDRKAI 280  
 QY 258 AKKOICPIVSMLEKELY 274  
 Db 281 GKKOIFCFASMLTKLFF 297

## RESULT 14

09D089 PRELIMINARY: PRT; 276 AA.  
 AC 09D089; 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE 10 days embryo cDNA, RIKEN full-length enriched library,  
 clone:2610037G10, full insert sequence.  
 GN CASP6.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=EMBRYO;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,  
 Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 Fleischmann M., Gasterland T., Gissi C., King B., Kochiwa H.,  
 Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
 Schimi L.M., Stabill F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,  
 Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 Brownstein M.J., Bult C., Fletcher C., Fujita K., Gariboldi M.,  
 Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 Suzuki H., Toyokawa K., Wang K.H., Weitz C., Whitlaker C., Wilming L.,  
 Wysshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
 Hayashizaki Y.;  
 RA "Functional annotation of a full-length mouse cDNA collection."  
 RT Nature 409:685-690(2001).  
 RL EMBL: AK011710; BAB27792.1; -  
 DR HSSP: P42574; 1PAU.  
 DR MGD: MGI:1312921; Casp6.  
 DR InterPro: IPR002398; ICE.  
 DR InterPro: IPR001309; ICE\_p10.  
 DR InterPro: IPR001309; ICE\_p20.  
 DR Pfam: PF00655; ICE\_p10; 1.  
 DR Pfam: PF00655; ICE\_p20; 1.  
 DR PRINTS: PR00376; ILBCEZYME.  
 DR SMART: SM00115; CASG; 1.  
 DR PROSITE: PS01122; CASPASE\_CYS; 1.  
 DR PROSITE: PS01121; CASPASE\_HIS; 1.  
 DR PROSITE: PS50207; CASPASE\_P10; 1.  
 DR PROSITE: PS50208; CASPASE\_P20; 1.  
 SQ SEQUENCE 276 AA; 31591 MW; 597EDF2321126B6C CRC64;

Query Match 35.3%; Score 516; DB 11; Length 276;  
 Best Local Similarity 41.0%; Pred. No. 2, 6e-35;  
 Matches 103; Conservative 42; Mismatches 94; Indels 12; Gaps 1;

QY 37 YKMDYPMGICITINNNKFNKSTGTSRSGTDVDANLRETFNKLKVEVNRKNDLTFREI 96  
 Db 20 YKMDHRRGVALIFNHRFFWHLTLPERGTNDRLTRRFSDLGEVXCFNDLRAEL 79

QY 97 VELNRDYSKEDHSKRSPVCYLLSHGEGILFGTMGPVDLKITNPFGRDRLSLTGPK 156  
 Db 80 LKTIHEVSTSSHIDADDICVFLSHGEGNHVAYADAKIEITQLTFLPKGCKQSLVGRK 139  
 QY 157 LFIIOACRGTLDCGIEFDSGD-----DDMACRHPVEADFLYASTAPGY 204  
 Db 140 IFTIOACRGSQHDVYVPLDMVDTKLDVNTQYDASVITLPGADFLMICYSAEGY 199  
 QY 205 SWRNSKDSWFIQSLCAMLKQYADKLEFPHILTRVNRKVAITEEFSFDPATFHAKQIPC 264  
 Db 200 SHRETVNGSVYIDLCVAVKAVASLEFTEILLVNRKVSORSVEYCNDRKAI 259  
 QY 265 IVSMLEKELY 275  
 Db 260 FASMLTKLFF 270

## RESULT 15

093415 PRELIMINARY: PRT; 304 AA.  
 AC 093415; 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Caspase-6.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20149872; PubMed=10684799;  
 RA Johnson A.L., Bridgman J.T.;  
 RT "Caspase-3 and -6 expression and enzyme activity in hen granulosa  
 cells."  
 RL Biol. Reprod. 62:589-598(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=11953316;  
 RA Ruchaud S., Korfall N., Villa P., Kotke T.J., Dingwall C.,  
 Kaufman S.H., Earnshaw W.C.;  
 RT "Caspase-6 gene disruption reveals a requirement for lamina A cleavage  
 in apoptotic chromatin condensation."  
 RL EMBO J. 21:1967-1977(2002).  
 DR EMBL: AF082329; AAC32378.1; -  
 DR EMBL: AF469049; AAL82386.1; -  
 DR HSSP: P42574; 1PAU.  
 DR MEROPS: C14.005; -  
 DR InterPro: IPR002398; ICE.  
 DR InterPro: IPR002138; ICE\_p10.  
 DR InterPro: IPR001309; ICE\_p20.  
 DR Pfam: PF00655; ICE\_p10; 1.  
 DR Pfam: PF00655; ICE\_p20; 1.  
 DR PRINTS: PR00376; ILBCEZYME.  
 DR SMART: SM00115; CASG; 1.  
 DR PROSITE: PS01122; CASPASE\_CYS; 1.  
 DR PROSITE: PS50207; CASPASE\_P10; 1.  
 DR PROSITE: PS50208; CASPASE\_P20; 1.  
 SQ SEQUENCE 304 AA; 34534 MW; 51CE31EBCAE7383 CRC64;

Query Match 35.2%; Score 515; DB 13; Length 304;  
 Best Local Similarity 40.5%; Pred. No. 3, 6e-35;  
 Matches 102; Conservative 46; Mismatches 92; Indels 12; Gaps 1;

QY 37 YKMDYPMGICITINNNKFNKSTGTSRSGTDVDANLRETFNKLKVEVNRKNDLTFREI 96  
 Db 49 YKMHQRGVALIFNHRFFWHLTLPERGTNDRLTRRFSDLGEVXCFNDLRAEDV 108  
 QY 97 VELNRDYSKEDHSKRSPVCYLLSHGEGILFGTMGPVDLKITNPFGRDRLSLTGPK 156  
 Db 109 LKKVEASRDYSNADFCVFLSHGEGNHVAYADAKIEITQLTFLPKGCKQSLVGRK 168

```

QY 157 LFIIOACRGTELDGCIETDSGVD-----DDMACHKIPVEADFLYASTAPGY 204
:|||||: | : | |
Db 169 IFIIACRGDDKHDPVLYQDSVDSKDETVNQTVEVDAGYTLFAGADFIHCYSVAQGT 228
QY 205 SWNSKDGSMFIOSLCAMLKQYADKLEFMHILTRVNRKVATEFESFSDATFHAQKQIPC 264
: | : : |||: | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 229 SHRETVNGSWYIODLCEALGKHGSSLEFTELLTVVNRKVSHRKVDICRDINAIGKKQIPC 288
QY 265 IVSMLTKELYFY 276
: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 289 FASMLTKKLYFH 300

```

Search completed: December 2, 2002, 12:58:11  
 Job time : 27.2672 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 2, 2002, 12:54:49 ; Search time 15.2828 seconds

(without alignments)  
1742.436 Million cell updates/sec

Title: US-09-895-263-4

Perfect score: 1463  
Sequence: 1 MENTENSVDSKSKINLEPKI.....AKQIPCIATSMLEKLYEVH 277

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: PIR\_73:\*

1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	1460	99.8	277 2	A55315
2	1308	89.4	277 2	S64710
3	1293	88.4	277 2	USC5410
4	996	68.1	212 2	167437
5	437	29.9	454 2	JC7123
6	418	28.6	416 2	G02635
7	381.5	26.1	503 2	A49429
8	352	24.1	495 2	T20038
9	328.5	22.5	435 2	A54821
10	327.5	22.4	452 2	JC6507
11	310.5	21.2	536 2	T43633
12	306.5	21.0	826 2	T43638
13	277	18.9	642 2	T27021
14	274.5	18.8	242 2	JC7517
15	247.5	16.9	402 2	A46495
16	246.5	16.8	377 2	A57511
17	232.5	15.9	418 2	T13385
18	230.5	15.8	488 2	T13385
19	230	15.7	182 2	167436
20	222.5	15.2	404 2	A2677
21	222	15.2	311 2	B56084
22	222	15.2	383 2	A56084
23	212	14.5	312 2	B54821
24	182	12.4	263 2	C56084
25	170.5	11.7	149 2	T43637
26	166	11.3	136 2	I53300
27	135.5	9.3	139 2	T43642
28	114.5	7.8	394 2	T26968
29	110	7.5	768 2	T18461

## ALIGNMENTS

30	100.5	6.9	457	2	T05439	hypothetical prote
31	96	6.6	537	2	I51592	protein-tyrosine k
32	93	6.4	534	1	S33568	protein-tyrosine k
33	92.5	6.3	525	2	T31677	bactiracin synthet
34	91.5	6.3	642	2	D88951	protein C38C3.7 (1
35	91	6.2	629	2	A62497	hypothetical prote
36	90.5	6.2	534	1	AA4991	protein-tyrosine k
37	89	6.1	2052	2	C97038	phage-related prot
38	88	6.0	537	1	TVHUSY	protein-tyrosine k
39	88	6.0	600	2	S28496	microtubule-associ
40	88	6.0	781	2	C69432	signal-transducing
41	88	6.0	1087	2	T30330	gelosolin-related p
42	87.5	6.0	299	2	D81384	probable lipoprote
43	87.5	6.0	552	2	S17551	gamma-aminobutyric
44	87.5	6.0	554	2	G01928	gamma-aminobutyric
45	87.5	6.0	556	2	S06838	gamma-aminobutyric

## RESULT 1

A55315  
Cysteine proteinase (EC 3.4.22.-) CPP32 precursor - human

N:Alternate names: cysteine proteinase CPP32  
C:Species: Homo sapiens (man)

C>Date: 06-Feb-1995 #sequence, revision 06-Feb-1995 #text, change 01-Dec-2000  
R:Accession: A55315; S58899; I39005  
R:Fernandes-Alnemrl, T.; Iltwack, G.; Alnemrl, E.S.

J. Biol. Chem. 269, 30761-30764, 1994  
A>Title: CPP32, a novel human apoptotic protein with homology to Caenorhabditis elegans

A:Reference number: A55315; M0ID:95074058; PMID:7983002  
A:Accession: A55315

A>Status: Preliminary  
A:Molecule type: mRNA

A:Residues: 1-277 <PER>  
A:Cross-references: GB:U13737; NID:9561665; PIDN:AAA65015.1; PID:9561666

R:Nicholson, D.W.; Ali, A.; Thornberry, N.A.; Vailancourt, J.P.; Ding, C.K.; Gallant  
; Yu, V.L.; Miller, D.K.

Nature 376, 37-43, 1995  
A>Title: Identification and inhibition of the ICE/CED-3 protease necessary for mammal

A:Reference number: S58899; M0ID:95319529; PMID:7596430  
A:Accession: S58899

A:Molecule type: protein  
A:Residues: 29-46;176-189, 'E', 191-193 <NIC>

R:Newari, M.; Quan, L.T.; O'Rourke, K.; Desnoyers, S.; Zeng, Z.; Beidler, D.R.; Polt  
Cell 81, 801-809, 1995  
A>Title: Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable proteas

A:Reference number: A56924; M0ID:95292347; PMID:7774019  
A:Accession: I39005

A>Status: Preliminary  
A:Molecule type: mRNA

A:Residues: 1-189, 'E', 191-277 <RES>  
A:Cross-references: EMBL:U26943; NID:9857568; PIDN:AAA74929.1; PID:9857569

C:Keywords: apoptosis; cysteine proteinase; hydrolase; lymphocyte  
Query Match

Best local similarity 99.8%; Score 1460; DB 2; Length 277;  
Matches 276; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	MENTENSVDSKSKINLEPKIHGSEMDSGISLDNSYKMDYPMGLCTIINNFHKSSTG	60
DB	1	MENTENSVDSKSKINLEPKIHGSEMDSGISLDNSYKMDYPMGLCTIINNFHKSSTG	60
QY	61	MNRSSTVDVDAANLRETFNRLKYEVRNKNDLREELVEIEMRDVSKSDHSRSSFVCYLLS	120
DB	61	MNRSSTVDVDAANLRETFNRLKYEVRNKNDLREELVEIEMRDVSKSDHSRSSFVCYLLS	120
QY	121	HEEEGIIFGTNGPVVDLKKITNFEGRDRSLTGKPKLFIIOACRGTELDGCIETDSGYDD	180
DB	121	HEEEGIIFGTNGPVVDLKKITNFEGRDRSLTGKPKLFIIOACRGTELDGCIETDSGYDD	180
QY	181	DMACHRIPEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVN	240



Biochem. Biophys. Res. Commun. 264, 550-555, 1999  
 A:Title: Akt phosphorylation site found in human caspase-9 is absent in mouse caspase-9  
 A:Reference number: JCT123; M0ID:20001956; PMID:10529400  
 A:Accession: JCT123  
 A:Status: preliminary  
 A:Molecule type: RNA  
 A:Residues: 1-454 <FNU>  
 A:Cross-references: DDBJ:AB019600; NID:96440941; PID:96440942

Query Match 29.9%; Score 437; DB 2; Length 454;  
 Best Local Similarity 36.1%; Pred. No. 7e-28;  
 Matches 99; Conservative 48; Mismatches 85; Indels 42; Gaps 6;

QY 34 DNSYKMDYEMGLCTIINKNFKSTGMSRSTVDAAALRETFRLKTEVNRKNDLTR 93  
 Db 188 DMAVYTLSDPCGCHLITNNVNFCSRSGSLGRITGNSIDRDLERFRMLREVEKKNDLTA 247  
 QY 94 EEIVELMRVSKEDHRSFVCLLSHGE-----GIIFGTNG-PVYLKKTITNFERG 145  
 Db 248 KKMVTRALMMAHRNHALDCFFVYIILSHGQASHLOFPQAVYTGDCSVSIEKIVNIFNG 307  
 QY 146 DRCRSLTGKPKLFITIOACRGTELDGIEF-----DSGVDDDM----- 182  
 Db 308 SGCPSLGGKPKLFITIOACGEGEKDHGFVACSTSSQGRITLSDSEDPATPREGPRPLDQL 367  
 QY 183 -ACHKIPVADFLYASTAPGYTSMRNSKDGSMFIOSLCAMLKQYADKLEFMHILTRVNR 241  
 Db 368 DAVSSLPSPSDILVSTFPGFVSMRDKKSGSWYIEILDGILQFWARSEDLQSLILRVAN 427  
 QY 242 KVATEFESEFPDTPFAKKOIPCTIVMLTKELF 275  
 Db 428 AVSEK-----GTY---KQIPCEFNFLRKLKF 451

# RESULT 6

G02635  
 ICE-LAP6 - human  
 C:Species: Homo sapiens (man)  
 C:Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 05-Nov-1999  
 A:Accession: G02635  
 R:Date: H.; Orth, K.; Chinnaiyan, A.M.; Polier, G.G.; Froelich, C.J.; He, W.W.; Dixit, submitted to the EMBL Data Library, April 1996  
 A:Reference number: H01513  
 A:Accession: G02635  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-416 <DNA>  
 A:Cross-references: EMBL:U56390; NID:91336026; PIDN:AAC50640.1; PID:91336027

Query Match 28.6%; Score 418; DB 2; Length 416;  
 Best Local Similarity 33.2%; Pred. No. 2.2e-26;  
 Matches 91; Conservative 51; Mismatches 90; Indels 42; Gaps 4;

QY 34 DNSYKMDYEMGLCTIINKNFKSTGMSRSTVDAAALRETFRLKTEVNRKNDLTR 93  
 Db 150 DAYILSMPCCHLITNNVNFCSRSGSLGRITGNSIDRDLERFRMLREVEKKNDLTA 209  
 QY 94 EEIVELMRVSKEDHRSFVCLLSHGE-----GIIFGTNG-PVYLKKTITNFERG 145  
 Db 210 KKMVTRALMMAHRNHALDCFFVYIILSHGQASHLOFPQAVYTGDCSVSIEKIVNIFNG 289  
 QY 146 DRCRSLTGKPKLFITIOACRGTELDGIEFDSGVDDDM----- 182  
 Db 270 TSCPSLGGKPKLFITIOACGEGEKDHGFVACSTSSQGRITLSDSEDPATPREGPRPLDQL 329  
 QY 183 -ACHKIPVADFLYASTAPGYTSMRNSKDGSMFIOSLCAMLKQYADKLEFMHILTRVNR 241  
 Db 330 DAVSSLPSPSDILVSTFPGFVSMRDKKSGSWYIEILDGILQFWARSEDLQSLILRVAN 389  
 QY 242 KVATEFESEFPDTPFAKKOIPCTIVMLTKELF 275  
 Db 390 AVSEK-----GIYKQMGCFNFKLKF 413

RESULT 7  
 A49429  
 Interleukin-1 beta-converting enzyme homolog CED-3 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 07-Apr-1994 #sequence\_revision 18-Nov-1994 #text\_change 01-Dec-2000  
 A:Accession: A49429; T37312  
 R:Yuan, J.; Shih, S.; Ledoux, S.; Ellis, H.M.; Horvitz, H.R.  
 Cell 75, 641-652, 1993  
 A:Title: The C. elegans cell death gene ced-3 encodes a protein similar to mammalian  
 A:Reference number: A49429; M0ID:94061982; PMID:8242740  
 A:Accession: A49429  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-503 <YUA>  
 A:Cross-references: GB:U29052; NID:96503232; PIDN:AAA27982.2; PID:96503233  
 A:Note: sequence extracted from NCBI backbone (NCBI:139825, NCBI:139826)  
 A:Accession: T37312  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-417, R, 419-503 <YU2>  
 A:Cross-references: EMBL:U29052; PIDN:AAA27982.1  
 C:Genetics:  
 A:Gene: ced-3  
 A:Introns: 45/3; 94/2; 179/1; 289/3; 361/1; 403/3; 483/3

Query Match 26.1%; Score 381.5; DB 2; Length 503;  
 Best Local Similarity 31.7%; Pred. No. 2.6e-23;  
 Matches 96; Conservative 50; Mismatches 108; Indels 49; Gaps 8;

QY 2 ENTENSVDSIKNLEKIIHGSMDSGISLDSYKMDYEMGLCTIINKNFKSTG 61  
 Db 214 EEDMNFVADAPTISR-----VFDEKTM-----YRFSSPRMCLITNNEHQ---M 256  
 QY 62 TNRSGTVDAAALRETFRLKTEVNRKNDLTRFEEIVELMRVSKEDHRSFVCLLSH 121  
 Db 257 PIRNGTRADKNDLNLFRCKGYTYICKDNLGRGMLTIRPFAHE-SHGDAIILVILSH 315  
 QY 122 GEEGIIIFGTNG-PVYLKKTITNFERGDCRSITGKPKLFITIOACRGTELDGIEFDSGV 179  
 Db 316 GEEVILIGVDIPISTHEIYDLNANAPRANKPKLVQACGGERDNGFVLDSVDG 375  
 QY 180 -----DDMAC-----HKIPVADFLYASTAPGYTSMRNSKDG 213  
 Db 376 VPALRRGMNDRGPLENFGCVAPQYQVWRKKPSOADIILAVATTAQYVSMRNSARG 435  
 QY 214 WFIOSLCAMLKQYADKLEFMHILTRVNRKVATEFESEFPDTPFAKKOIPCTIVMLTKEL 273  
 Db 436 WFIQAVCEVSTHAKMDVLLTEVNRKVAACGQT--SOGSNILKOMPMTSLRKLKF 492  
 QY 274 YFY 276  
 Db 493 YFW 495

# RESULT 8

T20038  
 hypothetical protein C48D1.2 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 A:Accession: T20038  
 R:Burton, J.  
 submitted to the EMBL Data Library, October 1996  
 A:Reference number: Z19214  
 A:Accession: T20038  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-495 <WIL>  
 A:Cross-references: EMBL:Z81049; PIDN:CAB02848.1; GSPDB:GN00022; CESP:C48D1.2  
 A:Experimental source: clone C48D1  
 C:Genetics:  
 A:Gene: CESP:C48D1.2  
 A:Map position: 4







QY 204 YSMRNSKDSGSMFIOISLCAMLKOYADKLEFMHILTRVNRKVATFESFSPATFHAQKQIP 263  
 Db 176 IAYRHDOGSCFIOQLVDFETK--RKGHILELLETVTRRMA-EAEVLQ---ECKARKTNP 229  
 QY 264 CIVSMUTKELY 274  
 Db 230 EIQSTLRKRLY 240

## RESULT 15

A46495

IL-1 beta convertase - mouse

C:Species: Mus musculus (house mouse)

C:Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 01-Dec-2000

C:Accession: A46495; A47258; I48911

R:Nett, M.A.; Gerretti, D.P.; Berson, D.R.; Seavitt, J.; Gilbert, D.J.; Jenkins, N.A.; C

J. Immunol. 149, 3254-3259, 1992.

A:Title: Molecular cloning of the murine IL-1 beta converting enzyme cDNA.

A:Reference number: A46495; MUID:93056487; PMID:1431103

A:Accession: A46495

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-402 &lt;NET&gt;

A:Cross-references: GB:I03799; NID:q198379; PIDN:AAA39306.1; PID:q198380

A:Note: Sequence extracted from NCBI backbone (NCBIP:117473)

R:Mollineaux, S.M.; Casano, F.J.; Rolando, A.M.; Peterson, E.P.; Lamjuco, G.; Chin, J.; C

ard, A.D.; Thornberry, N.A.; Kostura, M.J.

Proc. Natl. Acad. Sci. U.S.A. 90, 1809-1813, 1993

A:Title: Interleukin 1 beta (IL-1 beta) processing in murine macrophages requires a stru

A:Reference number: A47258; MUID:93189587; PMID:8446594

A:Accession: A47258

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-187, 189-402 &lt;MOL&gt;

A:Experimental source: macrophage

A:Note: Sequence extracted from NCBI backbone (NCBIP:126931)

R:Casano, F.J.; Rolando, A.M.; Mudgett, J.S.; Mollineaux, S.M.

Genomics 20, 474-481, 1994

A:Title: The structure and complete nucleotide sequence of the murine gene encoding Inte

A:Reference number: A54264; MUID:94307735; PMID:8034321

A:Accession: I48911

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 'MAV', 7-402 &lt;RES&gt;

A:Cross-references: EMBL:U04269; NID:q476217; PIDN:AAA56992.1; PID:q476218

C:Genetics:

A:Introns: 6/1; 92/1; 113/1; 150/3; 208/3; 287/1; 334/1; 370/3

Query Match

16.9%; Score 247.5; DB 2; Length 402;

Best Local Similarity 29.0%; Pred. No. 1.6e-12;

Matches 88; Conservative 46; Mismatches 124; Indels 45; Gaps 11;

QY 6 NSVDSKSIKNIPEKTIHSESDSISLDSNYKM-----DYPEMG-----LCITINN 52  
 Db 110 SSSSEKREONKEDGTFPGTLGTLPCKPLEKQKWKENSEIYPIIMNTTTRTLALICN 169  
 QY 53 KNFEKSTGMTSRSGTDVDAANLRETFRNLYEVNRKNNDLREIYELMRDYSK-EDHSKR 111  
 Db 170 TEFQH---LSRPVGAQVLDREKLLLEDIGTYVKKYKENITALEMVKYKERAACEPHKTS 226  
 QY 112 SSFVCVLLSHG-EEGIIFGT--NGPVDLKITNFR--GDRCSLTGKPKLFIIOACRG 165  
 Db 227 DSTFLVFMHSHGIEGICGTYTSNEVSDILKVDITIFQMMNTLCPSLKDKPKVITIIQACRG 286  
 QY 166 TELDQGITDS-----GVDDMAACHKIPYEADEFIAYSTAPGYYSNRNSKDSG 214  
 Db 287 EKQGVLLKDDVRSDEDFLDALPEEDGKIKRAHEKDFIACSSPTDVMVSRHPYRGSL 346  
 QY 215 FIOSLCAMLKOYADKLEFMHILTRVNRKVATFESFSPATFHAQKQIPCIYSM-LTKEL 273  
 Db 347 FIESLIKMKREYAMSCD---LEDIFRKVYRPSFEOPEF-----RLQMPTRADVITLTKRF 396

QY 274 YFY 276  
 Db 397 YLF 399  
 Search completed: December 2, 2002, 12:57:09  
 Job time: 17.2828 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 2, 2002, 12:54:49 ; Search time 9.55172 Seconds

(without alignments)  
1202,814 Million cell updates/sec

Title: US-09-895-263-4

Perfect score: 1463

Sequence: 1 MENTENSVDKSIKMLEPKI.....AKKOIPCVSMLEKLYFYH 277

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1460	99.8	277	1	ICE3_HUMAN
2	1317	90.0	277	1	ICE3_RAT
3	1293	88.4	277	1	ICE3_CRLO
4	1293	88.4	277	1	ICE3_MOUSE
5	786.5	53.8	282	1	ICE3_XENLA
6	748.5	51.2	303	1	ICE7_MOUSE
7	726.5	49.7	303	1	ICE7_MSAU
8	726.5	49.6	303	1	ICE7_HUMAN
9	526	36.0	276	1	ICE6_MOUSE
10	517.5	35.4	293	1	ICE6_HUMAN
11	502.5	34.3	339	1	ICE_DROME
12	470	32.1	299	1	ICE1_SPROF
13	469	32.1	323	1	ICE1_HUMAN
14	421	28.8	479	1	ICE8_HUMAN
15	410	28.0	503	1	ICE9_HUMAN
16	381.5	26.1	516	1	CEB3_CAEEL
17	362	24.7	496	1	CEB3_CAEVU
18	356.5	24.4	424	1	ICE2_CHICK
19	336.5	23.0	435	1	ICE2_MOUSE
20	328.5	22.5	435	1	ICE2_HUMAN
21	321	21.9	521	1	ICEA_HUMAN
22	274.5	18.8	242	1	ICEE_MOUSE
23	274	18.7	257	1	ICER_MOUSE
24	266.5	18.2	386	1	ICER_XENLA
25	265.5	18.1	410	1	ILBC_FELCA
26	259.5	17.7	382	1	ICER_XENLA
27	254.5	17.4	419	1	ICER_MOUSE
28	253	17.3	402	1	ILBC_RAT
29	250	17.1	405	1	ILBC_HORSE
30	247.5	16.9	402	1	ILBC_MOUSE
31	246.5	16.8	377	1	ICE4_HUMAN
32	239	16.3	312	1	ICE2_RAT
33	235.5	16.1	377	1	ICE2_BOVIN

34	234.5	16.0	404	1	ILBC_CANPA
35	232.5	15.9	418	1	ICES_HUMAN
36	222.5	15.2	404	1	ILBC_HUMAN
37	217.5	14.9	373	1	ICEB_MOUSE
38	213.5	14.6	404	1	ILBC_PIG
39	202	13.8	484	1	CFLA_MOUSE
40	183	12.5	480	1	CFLA_HUMAN
41	96	6.6	536	1	FYN_XIPHE
42	93	6.4	533	1	FYN_CHICK
43	92.5	6.3	5255	1	BACA_BACLI
44	90.5	6.2	533	1	FYN_MOUSE
45	88	6.0	536	1	FYN_HUMAN

## ALIGNMENTS

RESULT 1  
ICE3\_HUMAN STANDARD: PRT: 277 AA.  
AC P42574.  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Apoptain precursor (PC 3.4.22.-) (Cysteine protease CPP32) (Yama protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1) (SCA-1).  
DE (SCA-1).  
GN CASP3 OR CPP32.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ALPHA AND BETA ISOFORMS).  
RC TISSUE=T-cell;  
RX MEDLINE=95074098; PubMed=7983002;  
RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;  
RT "CPP32, a novel human apoptotic protein with homology to Interleukin-1 beta-converting enzyme."  
RT J. Biol. Chem. 269:30761-30764(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95292347; PubMed=7774019;  
RA Tewari M., Quan L.T., O'Rourke K., Desnoyers S., Zeng Z.,  
RA Beidler D.R., Poirier G.G., Salvesen G.S., Dixit V.M.;  
RT "Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable protease that cleaves the death substrate poly(ADP-ribose)."  
RT Cell 81:801-809(1995).  
RN [3]  
RP SEQUENCE OF 29-46 AND 175-193, AND FUNCTION.  
RX MEDLINE=95319529; PubMed=7596430;  
RA Nicholson D.W., Ali A., Thornberry N.A., Viallanco J.P., Ding C.K.,  
RA Gallant M., Gareau Y., Griffin P.R., Labelle M., Lazebnik Y.A.,  
RA Munday N.A., Ray S.M., Smulson M.E., Yamin T.-T., Li V.L.,  
RA Miller D.K.;  
RT "Identification and inhibition of the ICE/CED-3 protease necessary for mammalian apoptosis."  
RT Nature 376:37-43(1995).  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 28-277.  
RX MEDLINE=9626352; PubMed=8673606;  
RA Rionda J., Nicholson D.W., Fazil K.M., Gallant M., Gareau Y.,  
RA Labelle M., Peterson E.P., Rasper D.M., Ruel R., Viallanco J.P.,  
RA Thornberry N.A., Becker J.W.;  
RT "The three-dimensional structure of apoptin/CPP32, a key mediator of apoptosis."  
RT Nat. Struct. Biol. 3:619-625(1996).  
RN [5]  
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 35-173 AND 185-277.  
RX MEDLINE=97197830; PubMed=9045680;  
RA Mittl P.R., di Marco S., Krebs J.F., Bai X., Karanewsky D.S.,

RA Priestle J.P., Tomasselli K.J., Grutter M.G.:  
RT "Structure of recombinant human CPP32 in complex with the  
RL tetrapeptide acetyl-Asp-Val-Ala-Asp fluoromethyl ketone."  
J. Biol. Chem. 272:6539-6547(1997).  
[6]  
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).  
RX MEDLINE=20283632; PubMed=10821855;  
RA Lee D., Long S.A., Adams J.L., Chan G., Vaidya K.S., Francis T.A.,  
RA Kikly K., Winkler J.D., Sung C.M., Debouck C., Richardson S.,  
RA Levy M.A., Demelf W.E., Jr., Keller P.M., Tomaszek T., Head M.S.,  
RA Ryan M.D., Hallwanger R.C., Liang P.H., Janson C.A., McDevitt P.J.,  
RA Johnson K., Concha N.O., Chan W., Abdel-Meguid S.S., Badger A.M.,  
RA Lark M.W., Nadeau D.P., Suva L.J., Gowen M., Nuttall M.E.:  
RT "Potent and selective nonpeptide inhibitors of caspases 3 and 7  
inhibit apoptosis and maintain cell functionality."  
J. Biol. Chem. 275:16007-16014(2000).  
[7]  
RP PROCESSING.  
RX MEDLINE=96353838; PubMed=8755496;  
RA Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,  
RA Wang L., Bullrich F., Frits L.C., Trapani J.A., Tomasselli K.J.,  
RA Litwack G., Alnemri E.S.:  
RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human  
apoptotic cysteine protease containing two FADD-like domains."  
Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).  
[8]  
RP CLEAVAGE OF HUNTINGTIN.  
RX MEDLINE=96331285; PubMed=8696339;  
RA Goldberg Y.P., Nicholson D.W., Rasper D.M., Kalchauer M.A., Kolde H.B.,  
RA Graham R.K., Bromm M., Kazemi-Esfarjani P., Thornberry N.A.,  
RA Vallancourt J.P., Hayden M.R.:  
RT "Cleavage of huntingtin by apoptosis, a proapoptotic cysteine protease,  
is modulated by the polyglutamine tract."  
Nat. Genet. 13:442-449(1996).  
-1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES  
RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT  
PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A  
216-ASP-1-GLY-217 BOND. CLEAVES AND ACTIVATES SEROL REGULATOR  
ELEMENT BINDING PROTEINS (SREBPS) BETWEEN THE BASIC HELIX-LOOP-  
HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.  
CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9. INVOLVED IN THE  
CLEAVAGE OF HUNTINGTIN.  
-1- ENZYME REGULATION: INHIBITED BY ISATIN SULFONAMIDES.  
-1- SUBUNIT: HETERODIMER OF A 17 kDa (P17) AND A 12 kDa (P12) SUBUNIT.  
-1- SUBCELLULAR LOCATION: Cytoplasmic.  
-1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, SPLEEN, HEART, LIVER  
AND KIDNEY. MODERATE LEVELS IN BRAIN AND SKELETAL MUSCLE, AND LOW  
IN TESTIS. ALSO FOUND IN MANY CELL LINES. HIGHEST EXPRESSION IN  
CELLS OF THE IMMUNE SYSTEM.  
-1- PTM: CLEAVAGE BY GRANZYME B, APAF-1, CASPASE-6, -8 AND -10  
GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE  
PROPEPTIDES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE  
ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT  
OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR  
AND VICE VERSA.  
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.  
-----  
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CC or send an email to [license@sdb-sdb.ch](mailto:license@sdb-sdb.ch)).  
CC  
CC EMBL, U13737; AA65015.1;  
CC EMBL, U13738; AA60355.1;  
CC EMBL, U26943; AA74929.1;  
CC PDB, 1PAU; 07-JUL-97.  
CC PDB, 1CP3; 24-DEC-97.  
CC PDB, 1GFV; 23-JUN-00.  
CC MEROPS; C14.003;  
CC Genew; HGNC:1504; CASP3.

DR MM, 600636;  
DR InterPro: IPR002398; ICE.  
DR InterPro: IPR002138; ICE\_P10.  
DR InterPro: IPR001309; ICE\_P20.  
DR Pfam: PF00655; ICE\_P10; 1.  
DR Pfam: PF00656; ICE\_P20; 1.  
DR PRINTS: PR00376; ILICENZYME.  
DR SMART: SM00115; CASP. 1.  
DR PROSITE: PS01122; CASPASE\_CYS. 1.  
DR PROSITE: PS01121; CASPASE\_HIS. 1.  
DR PROSITE: PS50207; CASPASE\_P10; 1.  
DR PROSITE: PS50208; CASPASE\_P20; 1.  
KW Hydroxylase; Thiol protease; Caspase; P20; 1.  
KW 3D-structure.  
FT PROPEP 1 9  
FT PROPEP 10 28  
FT CHAIN 29 175 APOPAIN P17 SUBUNIT.  
FT CHAIN 176 277 APOPAIN P12 SUBUNIT.  
FT ACT\_SITE 121 121 BY SIMILARITY.  
FT ACT\_SITE 163 163 BY SIMILARITY.  
FT VARIANT 190 190 D->E (IN ISOFORM BETA).  
FT  
SQ SEQUENCE 277 AA; 31594 MW; 8E34DD2ACE6E64B CRC64;  
/FTID=VAR\_001401.  
Query Match 99.8%; Score 1460; DB 1; Length 277;  
Best Local Similarity 99.6%; Pred. No. 1.7e-115;  
Matches 276; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MENTENSVDKSIKLEPKIIGSEMSDGSISLNSYKMDYPMGLCTIINKNFHKGSTG 60  
DB 1 MENTENVDSKSIKLEPKIIGSEMSDGSISLNSYKMDYPMGLCTIINKNFHKGSTG 60  
QY 61 MTSRSGTDVDAANLRETFRLNLYEVNRKNDITREIYELMRDVSKEHSSKRSFVCVLLS 120  
DB 61 MTSRSGTDVDAANLRETFRLNLYEVNRKNDITREIYELMRDVSKEHSSKRSFVCVLLS 120  
QY 121 HGEIGIIFGNGPVDLKKINFFRGDCRSITGPKLFIIOACGTGLDGIETDGSVDD 180  
DB 121 HGEIGIIFGNGPVDLKKINFFRGDCRSITGPKLFIIOACGTGLDGIETDGSVDD 180  
QY 181 DMACHKIPVADFLYASTAPGYSMRNSKDGSMFISLCLMLKQYADKLEFMIILFRVN 240  
DB 181 DMACHKIPVADFLYASTAPGYSMRNSKDGSMFISLCLMLKQYADKLEFMIILFRVN 240  
QY 241 RKVATFEFSFDPATFAKKOIPCIYVSLTKELFYFH 277  
DB 241 RKVATFEFSFDPATFAKKOIPCIYVSLTKELFYFH 277  
RESULT 2  
ICE3-RAT STANDARD; PRT; 277 AA.  
ID ICE3-RAT  
AC P55213; P70543; Q62993; P97699;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DE 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Apopain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama  
DE protein) (CPP-32) (Caspase-3) (SREBP cleavage activity 1)  
DE (SCA-1) (LICE) (IRP).  
GN CASP3 OR CPP32.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OC NCB1\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96358624; PubMed=8761296;  
RA Juan T.S.-C., McNiece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G.,  
RA Fletcher F.A.:  
RT "Molecular characterization of mouse and rat CPP32 beta gene encoding  
RT a cysteine protease resembling interleukin-1 beta converting enzyme  
RT and CED-3."  
RT Oncogene 13:749-755(1996).

RN [2]  
 RP SEQUENCE OF 30-241 FROM N.A.  
 RC TISSUE-Ovary; PubMed-7588240;  
 RX MEDLINE-96042508; PubMed-7588240;  
 RA Flaws J.A., Kugu K., Tribovich A.M., Desanti A., Tilly K.I.,  
 RA Hirschfeld A.N., Tilly J.L.;  
 RT "Interleukin-1 beta-converting enzyme-related proteases (IRPs) and  
 RT mammalian cell death: dissociation of IRP-induced oligonucleosomal  
 RT endonuclease activity from morphological apoptosis in granulosa cells  
 RT of the ovarian follicle.";  
 RL Endocrinology 136:5042-5053(1995).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Brain;  
 RX MEDLINE-97184204; PubMed-9030616;  
 RA Ni B., Wu X., Du Y., Su Y., Hamilton-Byrd E., Rockey P.K.,  
 RA Rostack P. Jr., Polster G.G., Paul S.M.;  
 RT "Cloning and expression of a rat brain interleukin-1-beta-converting  
 RT enzyme (ICE)-related protease (IRP) and its possible role in  
 RT apoptosis of cultured cerebellar granule neurons.";  
 RL J. Neurosci. 17:1561-1569(1997).  
 RN [4]  
 RP SEQUENCE OF 1-264 FROM N.A.  
 RA Yakovlev A.G.;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES  
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT  
 CC PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A  
 CC 216-ASP-1-GLY-217 BOND. CLEAVES AND ACTIVATES STEROL REGULATORY  
 CC ELEMENT BINDING PROTEINS (SREBPS) BETWEEN THE BASIC HELIX-LOOP-  
 CC HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.  
 CC CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9 (BY SIMILARITY).  
 CC -1- SUBUNIT: HETERODIMER OF A 17 Kda (P17) AND A 12 Kda (P12) SUBUNIT  
 CC (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, LIVER, AND MUSCLE  
 CC BUT NOT IN KIDNEY OR TESTIS.  
 CC -1- DEVELOPMENTAL STAGE: HIGHLY EXPRESSED IN NEURON-ENRICHED REGIONS  
 CC OF THE DEVELOPING BRAIN, BUT DOWN-REGULATED TO LOW LEVELS IN THE  
 CC ADULT BRAIN.  
 CC -1- PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE  
 CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS  
 CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED  
 CC PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF  
 CC CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND  
 CC VICE VERSA (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.  
 CC -----  
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 CC or send an email to [license@sdb.ch](mailto:license@sdb.ch)).  
 CC -----  
 DR EMBL; U49930; AAC52765.1; -;  
 DR EMBL; U34685; AAC52261.1; -;  
 DR EMBL; U84410; AAB41792.1; -;  
 DR EMBL; U58656; AAB02722.1; -;  
 DR HSSP; P42574; 1PAU.  
 DR MEROPS; C14.003; -;  
 DR InterPro; IPR002398; ICE.  
 DR InterPro; IPR002138; ICE\_p10.  
 DR InterPro; IPR001309; ICE\_p20.  
 DR Pfam; PF00655; ICE\_p10; 1.  
 DR Pfam; PF00655; ICE\_p20; 1.  
 DR PRINTS; PR00376; ILIBENZNYME.  
 DR SMART; SM00115; CASc; 1.  
 DR PROSITE; PS01122; CASPASE\_CYS; 1.  
 DR PROSITE; PS01121; CASPASE\_HIS; 1.  
 DR PROSITE; PS50207; CASPASE\_P10; 1.  
 DR PROSITE; PS50208; CASPASE\_P20; 1.

KW Hydrolyase; Thiol protease; Zymogen; Apoptosis.  
 FT PROPEP 1 9  
 FT PROPEP 10 28  
 FT CHAIN 29 175  
 FT CHAIN 176 277  
 FT ACT\_SITE 121 121  
 FT ACT\_SITE 121 121  
 FT ACT\_SITE 163 163  
 FT CONFLICT 25 29  
 FT CONFLICT 170 170  
 FT CONFLICT 178 178  
 FT CONFLICT 182 182  
 FT CONFLICT 187 187  
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 FT CONFLICT 211 211  
 FT CONFLICT 236 236  
 FT CONFLICT 245 245  
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 FT CONFLICT 277 AA; 31491 MW; ADABF418E2507402 CRC64;  
 SO SEQUENCE  
 Query Match 90.0%; Score 1317; DB 1; Length 277;  
 Best Local Similarity 89.2%; Pred. No. 1.8e-103;  
 Matches 247; Conservative 13; Mismatches 17; Indels 0; Gaps 0;  
 QY 1 MENTENSVDKSKINLEPKIIGSESDSGISLDSYKMDYPENGCLTIINNNFKSTG 60  
 DB 1 MDNNETSVDSKINSINFEKTIHSGSKSDSGIYLSYKMDPEMGCLTIINNNFKSTG 60  
 QY 61 MTSAGSDVDVAANREFRNRIKYVRKNNDLTREIYELMADVSKEDSKSSFEVCVLLS 120  
 DB 61 MSANGSDVDVAANREFRNRIKYVRKNNDLTREIYELMADVSKEDSKSSFEVCVLLS 120  
 QY 121 HGEGLIFGTNGPVDLKITNFEFGDRCRSLTGKPKFIIOACGTETDGLIEDSGVD 180  
 DB 121 HGDEGVIFGTNGPVDLKITNFEFGDRCRSLTGKPKFIIOACGTETDGLIEDSGVD 180  
 QY 181 DMACHKIPVADFLYASTAGYVSNRNSKDGWFIOSLCAMLKQYADKLEFMHILFRVN 240  
 DB 181 DMACQKIPVADFLYASTAGYVSNRNSKDGWFIOSLCAMLKLYAHKLEFMHILFRVN 240  
 QY 241 RKVATEFESFSDATFPAKQIPCIYSMLTKELYFYH 277  
 DB 241 RKVATEFESFSDATFPAKQIPCIYSMLTKELYFYH 277  
 RESULT 3  
 ID ICE3\_CRILLO STANDARD; PRT; 277 AA.  
 AC 060431;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptin precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama  
 DE protein) (CPP-32) (Caspase-3) (SREBP cleavage activity 1)  
 DE (SCA-1).  
 GN CASP3 OR CPP32.  
 OS Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Cricetinae;  
 OC Cricetulus.  
 OX NCBI\_TaxID=10030;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Brain;  
 RX MEDLINE-96183185; PubMed-8605870;  
 RA Wang X., Zelenski N.G., Yang J., Sakai J., Brown M.S.,  
 RA Goldstein J.L.;  
 RT "Cleavage of sterol regulatory element binding proteins (SREBPs) by  
 RT CPP32 during apoptosis.";  
 RL EMO J. 15:1012-1020(1996).  
 CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES  
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT  
 CC PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A  
 CC 216-ASP-1-GLY-217 BOND. CLEAVES AND ACTIVATES STEROL REGULATORY

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CC ELEMENT BINDING PROTEINS (SREBPS) BETWEEN THE BASIC HELIX-LOOP-
CC HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.
CC CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9 (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF A 17 KDA (P17) AND A 12 KDA (P12) SUBUNIT
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- PTM: CLEAVAGE BY GRANTZYME B, CASPASE-6, -8 AND -10 GENERATES THE
CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
CC CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
CC VICE VERSA (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U27463; AAB01511.1; -.
DR HSRP: P42574; IPR0.
DR MEROPS: C14.003; -.
DR InterPro: IPR002398; ICE.
DR InterPro: IPR002138; ICE_P10.
DR InterPro: IPR001309; ICE_P20.
DR Pfam: PF00655; ICE_P10; 1.
DR Pfam: PF00656; ICE_P20; 1.
DR PRINTS: PR00376; ILIBCEZYME.
DR SMART: SM00115; CASC; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
DR Hydrolase: Thiol protease; Apoptosis.
KW PROPEP 1 9
FT PROPEP 10 28 BY SIMILARITY.
FT CHAIN 29 175 APOPTAIN P17 SUBUNIT.
FT ACT_SITE 176 277 APOPTAIN P12 SUBUNIT.
FT ACT_SITE 121 121 BY SIMILARITY.
FT ACT_SITE 163 163 BY SIMILARITY.
SQ SEQUENCE 277 AA; 31612 MW; 0BF3A4590A2828A3 CRC64;

Query Match 88.48; Score 1293; DB 1; Length 277;
Best Local Similarity 87.08; Pred. No. 1.8e-101;
Matches 241; Conservative 16; Mismatches 20; Indels 0; Gaps 0;

QY 1 MENTENSVDKSKINLEPKTIHSGESMDSGTSLDNTSYKMDYPMGGLCTIINKNFKHSTG 60
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QY 61 MTSRSGTDVDAANLRETFRNLYEVNRKNDLTREIYEIAMDVSKEHDSKRSFVCVLLS 120
DB 61 MTPRSGTDVDAAKLREFPMALKEVRKNDLTREIYEIELMKNASKEDHSKRSFVCVLLS 120
QY 121 HGEGBGIFGNGVDLKKITNFGRDRCRLTGKPKLFTIIOACRGTELDGCIETDGVDD 180
DB 121 HGEGBGIFGNGVDLKKITNFGRDRCRLTGKPKLFTIIOACRGTELDGCIETDGVDD 180
QY 181 DMACHKRPVADFLYASTAGYYSMRNSDGSFIOISLCAMLKQYADKLEFHHILRVN 240
DB 181 DMACHKRPVADFLYASTAGYYSMRNSDGSFIOISLCAMLKQYADKLEFHHILRVN 240
QY 241 RKVATEFESEFDPATFHAKKQIDPCTVSMLTRELYFYH 277
DB 241 RKVATEFESEFDPATFHAKKQIDPCTVSMLTRELYFYH 277

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AC P70677; 008668;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptin precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
DE protein) (CPP-32) (Caspase-3) (SREBP cleavage activity 1)
DE (SCA-1) (LICE).
DE CASP3 OR CPP32.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96358624; PubMed=8761296;
RA Juan T.S.-C., McNelece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G.,
RA Fletcher F.A.;
RT "Molecular characterization of mouse and rat CPP32 beta gene encoding
RT a cysteine protease resembling Interleukin-1 beta converting enzyme
RT and CED-3."
RL Oncogene 13:749-755(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97224429; PubMed=9070890;
RA Mukasa T., Urase K., Momoi M.Y., Kimura I., Momoi T.;
RT "Specific expression of CPP32 in sensory neurons of mouse embryos and
RT activation of CPP32 in the apoptosis induced by a withdrawal of
RT NGF."
RL Biochem. Biophys. Res. Commun. 231:770-774(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/An;
RX MEDLINE=97190206; PubMed=9038361;
RA van de Creen M., Vandenaebelle P., Declercq W., van den Brande I.,
RA van Looy G., Molens F., Schotte P., van Griekinge W., Beyaert R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members."
RL FEBS Lett. 403:61-69(1997).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
RT Submitted (May-1997) to the EMBL/Genbank/DBJ databases.
RL -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
CC RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT
CC PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PAR) AT A
CC 216-ASP-1-GLY-217 BOND. CLEAVES AND ACTIVATES STEROL REGULATORY
CC ELEMENT BINDING PROTEINS (SREBPS) BETWEEN THE BASIC HELIX-LOOP-
CC HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.
CC CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9 (BY SIMILARITY).
CC CLEAVES IL-1 BETA BETWEEN AN ASP AND AN ALA, RELEASING THE MATURE
CC CYTOKINE WHICH IS INVOLVED IN A VARIETY OF INFLAMMATORY PROCESSES.
CC -1- SUBUNIT: HETERODIMER OF A 17 KDA (P17) AND A 12 KDA (P12) SUBUNIT
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN SPLEEN, LUNG, LIVER,
CC KIDNEY AND HEART. LOWER EXPRESSION IN BRAIN, SKELETAL MUSCLE AND
CC TESTIS.
CC -1- PTM: CLEAVAGE BY GRANTZYME B, CASPASE-6, -8 AND -10 GENERATES THE
CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
CC PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CC CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
CC VICE VERSA (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC -----
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CC EMBL: U54803; AAC52768.1; -
DR EMBL: U54802; AAC52768.1; JOINED.
DR EMBL: U49929; AAC52768.1; -
DR EMBL: D86352; BAA21727.1; -
DR EMBL: Y13086; CAA3528.1; -
DR EMBL: U19522; AAC53196.1; -
DR HSSP: P42574; 1PAU.
DR MEROPS: C14.003; -
DR MGD: MGI:107739; Casp3.
DR InterPro: IPR002398; ICE.
DR InterPro: IPR002138; ICE_p10.
DR InterPro: IPR001309; ICE_p20.
DR Pfam: PF00655; ICE_p10; 1.
DR Pfam: PF00656; ICE_p20; 1.
DR PRINTS: PR00376; ILBENZYM.
DR SMART: SM00115; CASC; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
DR Hydrolase; Thiol protease; Zymogen; Apoptosis.
KW PROPEP 1 9
FT PROPEP 10 28
FT CHAIN 29 175
FT CHAIN 176 277
FT ACT_SITE 121 121
FT ACT_SITE 163 163
FT CONFLICT 51 51
FT CONFLICT 84 84
FT CONFLICT 95 95
FT CONFLICT 97 97
FT CONFLICT 128 128
FT CONFLICT 135 135
SQ SEQUENCE 277 AA; 31474 MW; CE91598F74826605 CRC64;

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Query Match 88.4%; Score 1293; DB 1; Length 277;
Best Local Similarity 86.6%; Pred. No. 1.8e-101;
Matches 240; Conservative 20; Mismatches 17; Indels 0; Gaps 0;

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QY 1 MENTNSVSKIKLEPPIIHGSESMDSGISLNDYKMDYEMGICITINNNKPKFKSTG 60
DB 1 MENTNTSDVSKINNENKATVHGSVSDGYLDSYKMDYEMGICITINNNKPKFKSTG 60
QY 61 MTSRSGTVDANLRETFNRLKYEVRNKNLDTREIIVELMRDYSKEDHSKRSFVCVLLS 120
DB 61 MSSRSGTVDANLRETFNRLKYEVRNKNLDTREIIVELMRDYSKEDHSKRSFVCVLLS 120
QY 121 HGEBCITFGNGPVDLKKITNFRRGDRCSLTGKPKLFTIOACRGTELDGSIETDSGVDD 180
DB 121 HGDEGVITGTNGPVLKLTSTFFRGDYCRSLTGKPKLFTIOACRGTELDGSIETDSGVDD 180
QY 181 DMACHKTIIVEADFLAYSTAPGYYSWRNSKDSWFIQSLCAMLKQYADKLEFMHILTRVN 240
DB 181 EMACKTIIVEADFLAYSTAPGYYSWRNSKDSWFIQSLCAMLKQYADKLEFMHILTRVN 240
QY 241 RKVATEFESFSDATFFHAKKOIPCIYVSMILTKELYFH 277
DB 241 RKVATEFESFSDATFFHAKKOIPCIYVSMILTKELYFH 277

RESULT 5
ID ICE3_XENLA STANDARD: PRT: 282 AA.
AC P55866:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (caspase-3)
DE (CASP-3) (XCP32).
GN CASP3
OS Xenopus laevis (African clawed frog).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97184166; PubMed=9030578;
RA Yaolta Y., Nakajima K.;
RT "Induction of apoptosis and CPP32 expression by thyroid hormone in a
RT myoblastic cell line derived from tadpole tail."
RL J. Biol. Chem. 272:5122-5127(1997)
CC -1- FUNCTION: IMPORTANT MEDIATOR OF APOPTOSIS. AT THE ONSET OF
CC APOPTOSIS IT PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE
CC (PARP) AT A 216-ASP-1-GLY-217 BOND (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF A 17 kDa (P17) AND A 12 kDa (P12)
CC SUBUNITS.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- MISCELLANEOUS: THE SUBUNITS ARE DERIVED FROM THE PRECURSOR
CC SEQUENCE BY A PROBABLE AUTOCATALYTIC MECHANISM AND PROBABLY BY
CC OTHER CASPASES (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D89784; BAA14018.1; -
DR HSSP: P42574; 1PAU.
DR MEROPS: C14.003; -
DR InterPro: IPR002398; ICE.
DR InterPro: IPR002138; ICE_p10.
DR InterPro: IPR001309; ICE_p20.
DR Pfam: PF00655; ICE_p10; 1.
DR Pfam: PF00656; ICE_p20; 1.
DR PRINTS: PR00376; ILBENZYM.
DR SMART: SM00115; CASC; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
KW Hydrolase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 186
FT CHAIN 187 282
FT ACT_SITE 131 131
FT ACT_SITE 174 174
SQ SEQUENCE 282 AA; 32124 MW; CB390E6980CAB77F CRC64;

Query Match 53.8%; Score 786.5; DB 1; Length 282;
Best Local Similarity 54.2%; Pred. No. 6.1e-59;
Matches 156; Conservative 40; Mismatches 73; Indels 19; Gaps 5;

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	Query Match	51.2%;	Score 748.5;	DB 1;	Length 303;
	Best Local Similarity	59.5%;	Pred. No. 1e-55;		
	Matches 144;	Conservative 36;	Mismatches 59;	Indels 3;	Gaps 1.
QY	37	YKMDYPENGGLIIINNNKHSTGMTSHSGTDVDANLRETFRNLKYEVRRNNDLTRREI	96		
Db	60	YRMDFOKMGKCIIINKNFEDKATGADVNRGTDKDAGALFRCFQNIGFEVTVINDSCAQM	119		
QY	97	VELMADYSEKHRSRSPVCYLISGEGEIIFGTGPVLDKITLWFFRDRCRLTGKR	156		
Db	120	QDLRKASEEDHSNACFCAYLLSGBEDLYGKGVPYPIKLTAHFRDDRCKTLLEKER	179		
QY	157	LFTIOACRGTELDGCIENDSGVDDDMAC---HKIVEADEFLYASTAGYSWRMSNKDS	213		
Db	180	LFETIACRGTELDGDIQADSGPINDIDANPNRKIEVEADEFLAYSTVPYYSWRMPGKS	239		
QY	214	WEIOSLCMLKOYADKLTFEMHILTPVNKKVATFEESFSFDAFHAKKOIPCLVSMLTREL	273		
Db	240	WFVOALCSILNEHGKDLEIMOLITLVNRVDRVAHFESQSDDPFNFKKOIPCMVSMILTREL	299		
QY	274	YF 275			
Db	300	YF 301			

RESULT 7	ICE7_MESAU	STANDARD:	PRT;	303 AA.
ID	ICE7_MESAU			
AC	P55214;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Caspase-7 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 3)			
DE	(ICE-LA43) (Apoptotic protease Mch-3) (SREBP cleavage activity 2)			
DE	(SCA-2)			
CN	CASP7 OR MCH3.			
OS	Mesocricetus auratus (golden hamster).			
OC	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;			
OC	Mesocricetus.			
OX	NCBI_TaxID=10036;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			

```

RC STRAIN=Syrian; TISSUE=Liver;
RX MEDLINE=96224303; PubMed=8643593;
RA Pat J.-T., Brown M.S., Goldstein J.L.;
RT "Purification and cDNA cloning of a second apoptosis-related cysteine
RT protease that cleaves and activates sterol regulatory element binding
RT proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 93:5437-5442(1996).
CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
CC RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES AND ACTIVATES STEROL
CC REGULATORY ELEMENT BINDING PROTEINS (SREBPS). PROTEOLYTICALLY
CC CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A 216-ASP-1-GLY-217
CC BOND. OVEREXPRESSION PROMOTES PROGRAMMED CELL DEATH (BY
CC SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF A 20 KDA (P20) AND A 11 KDA (P11) SUBUNIT
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- PTM: CLEAVAGES BY GRANTZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
CC SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
CC CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CC CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
CC VICE VERSA (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U47332; AAC52595.1; -.
DR HSSP: P42574; 1PAU.
DR MEROPS: C14.004; -.
DR InterPro: IPR002338; ICE.
DR InterPro: IPR001309; ICE_P20.
DR Pfam: PF00655; ICE_P10; 1.
DR Pfam: PF00656; ICE_P20; 1.
DR Pfam: PF00376; ILIBENZYME.
DR PRINTS: SM00115; CASC. 1.
DR SMART: SM00112; CASPASE_CYS. 1.
DR PROSITE: PS01121; CASPASE_HIS. 1.
DR PROSITE: PS01121; CASPASE_HIS. 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
DR HydroLase: Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 23
FT CHAIN 1 198 CASPASE-7 SUBUNIT P20.
FT PROPEP 199 206 BY SIMILARITY.
FT CHAIN 207 303 CASPASE-7 SUBUNIT P11.
FT ACT_SITE 144 144 BY SIMILARITY.
FT ACT_SITE 186 186 BY SIMILARITY.
SQ SEQUENCE 303 AA; 34037 MW; EA29355D9098448 CRC64;

Query Match 49.7%; Score 726.5; DB 1; Length 303;
Best Local Similarity 58.3%; Pred. No. 7,3e-54;
Matches 141; Conservative 35; Mismatches 63; Indels 3; Gaps 1;

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QY 274 YF 275
DB 300 YF 301

RESULT 8
ICE7_HUMAN
ID ICE7_HUMAN STANDARD; PRT; 303 AA.
AC P55210; 013364; 096BA0;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Caspase-7 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 3)
DE (ICE-LAP3) (Apoptotic protease Mch-3) (CMH-1).
GN CASP7 OR MCH3
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ALPHA ISOFORM).
RX MEDLINE=96139498; PubMed=8576161;
RA Duan H., Chinaiyan A.M., Hudson P.L., Wang J.P., He W.-W.,
RA Dixit V.M.;
RT "ICE-LAP3, a novel mammalian homologue of the Caenorhabditis elegans
RT cell death protein Ced-3 is activated during Fas- and tumor necrosis
RT factor-induced apoptosis."
RL J. Biol. Chem. 271:1621-1625(1996).
RN [2]
RP SEQUENCE FROM N.A. (ALPHA ISOFORM).
RX MEDLINE=96147144; PubMed=857622;
RA Lipke J.A., Gu Y., Sarnacki C., Caron P.R., Su M.S.-S.;
RT "Identification and characterization of CPP32/Mch2 homology 1, a novel
RT cysteine protease similar to CPP32."
RL J. Biol. Chem. 271:1825-1828(1996).
RN [3]
RP SEQUENCE FROM N.A. (ALPHA AND BETA ISOFORMS).
RX MEDLINE=96105019; PubMed=8521391;
RA Fernandez-Alnemir T., Takahashi A., Armstrong R.C., Krebs J.,
RA Fritz L.C., Tomasselli K.J., Wang L., Yu Z., Croce C.M., Salvson G.,
RA Earnshaw W.C., Litwack G., Alnemir E.S.;
RT "Mch3, a novel human apoptotic cysteine protease highly related to
RT CPP32."
RL Cancer Res. 55:6045-6052(1995).
RN [4]
RP SEQUENCE FROM N.A. (ALPHA AND ALPHA' ISOFORMS).
RX MEDLINE=97224489; PubMed=9070923;
RA Juan T.S.-C., McNiece I.K., Argento J.M., Jenkins N.A., Gilbert D.J.,
RA Copeland N.G., Fletcher F.A.;
RT "Identification and mapping of Casp7, a cysteine protease resembling
RT CPP32 beta, interleukin-1 beta converting enzyme, and CED-3."
RL Genomics 40:86-93(1997).
RN [5]
RP SEQUENCE FROM N.A. (ALPHA ISOFORM).
RX MEDLINE=9633838; PubMed=8755496;
RA Fernandes-Alnemir T., Armstrong R.C., Krebs J., Srinivasula S.M.,
RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomasselli K.J.,
RA Litwack G., Alnemir E.S.;
RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
RT apoptotic cysteine protease containing two FAD2-like domains."
RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
CC RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES AND ACTIVATES STEROL
CC REGULATORY ELEMENT BINDING PROTEINS (SREBPS). PROTEOLYTICALLY

```

CC CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A 216-ASP-1-GLY-217  
 CC BOND. OVEREXPRESSION PROMOTES PROGRAMMED CELL DEATH.  
 CC -1- ENZYME REGULATION: INHIBITED BY ISATIN SULFONAMIDES.  
 CC -1- SUBUNIT: HETERODIMER OF A 20 kDa (P20) AND A 11 kDa (P11) SUBUNIT.  
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.  
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: ALPHA (SHOWN HERE), BETA AND  
 CC ALPHA' ARE PRODUCED BY ALTERNATIVE SPLICING. THE BETA ISOFORM IS  
 CC NOT PROTEOLYTICALLY ACTIVE.  
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, SKELETAL MUSCLE,  
 CC LIVER, KIDNEY, SPLEEN AND HEART, AND MODERATELY IN TESTIS. NO  
 CC EXPRESSION IN THE BRAIN.  
 CC -1- PTM: CLEAVAGES BY GRANTZME B OR CASPASE-10 GENERATE THE TWO ACTIVE  
 CC SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY  
 CC CPP32 PROTEASE. ACTIVE HETERODIMER BETWEEN THE SMALL SUBUNIT OF  
 CC CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND  
 CC VICE VERSA.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.  
 CC -1- CAUTION: WHAT WE CALL ALPHA. ISOFORM IS KNOWN IN REF.4 AS BETA,  
 CC BUT AS BETA IS ALREADY DEFINED IN REF.3 WE HAVE CALLED IT ALPHA'.  
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 CC -----  
 CC EMBL: U39613; AAC50346.1; -  
 CC EMBL: U40281; AAC50352.1; -  
 CC EMBL: U37448; AAC50303.1; -  
 CC EMBL: U37449; AAC50304.1; -  
 CC EMBL: U67319; AAC51152.1; -  
 CC EMBL: U67320; AAC51153.1; -  
 CC EMBL: U67206; AAF21460.1; -  
 CC EMBL: BC015799; AAH15799.1; -  
 CC HSSP: P42574; IPAU.  
 CC MEROPS: C14.004; -  
 CC GeneW: HGNC:1508; CASP7.  
 CC MIM: 601761; -  
 CC InterPro: IPR002398; ICE.  
 CC InterPro: IPR002138; ICE\_P10.  
 CC InterPro: IPR001309; ICE\_P20.  
 CC Pfam: PF00655; ICE\_P10; 1.  
 CC Pfam: PF00656; ICE\_P20; 1.  
 CC PRINTS: PR00376; ILBCEZYME.  
 CC SMART: SM00115; CASC\_1.  
 CC PROSITE: PS01122; CASPASE\_CYS\_1.  
 CC PROSITE: PS01121; CASPASE\_HIS\_1.  
 CC PROSITE: PS50207; CASPASE\_P10; 1.  
 CC PROSITE: PS50208; CASPASE\_P20; 1.  
 CC HydroLase: Thiol protease; Zymogen; Apoptosis; Alternative splicing.  
 CC FT PROPEP 1 23  
 CC CHAIN 24 198  
 CC PROPEP 199 206  
 CC CHAIN 207 303  
 CC ACT\_SITE 144 144  
 CC ACT\_SITE 186 186  
 CC VARSPLIC 1 1  
 CC M -> MDCVGPMPGKMKLEKNTSCGGSSGICASYVTOM  
 CC (IN ISOFORM ALPHA').  
 CC VARSPLIC 149 303  
 CC VYGRDGYPIKDLTAHFGRGCKTLLEKPKLFQACRG  
 CC ELDDGIDQADSGPIINDTANPRKIVPEADLFVASTVPEY  
 CC SWRSPGSMFVQALCSLIEHKKDLEIMOLITRRNDPRAR  
 CC HFEOSDHPHEKQKQICVYSMLTKELYSO -> MESCS  
 CC VTAQGVQRDLGRLOPPPRPLKEGSLMAASPTGSPMTQ  
 CC MLIDTRSQMKLTSSSPITPQALTRGPGSGQAEAPGLCKRFA  
 CC PSMRSTKTKWSCRSSPG (IN ISOFORM BETA).  
 CC C -> A NO APOPTOTIC ACTIVITY.  
 CC D -> E (IN REF. 5).  
 CC G -> A (IN REF. 1).  
 CC MUTAGEN 186 186  
 CC CONFLICT 4 4  
 CC CONFLICT 194 194  
 CC SEQUENCE 303 AA: 34276 MW: CD373EE54A23CA4 CRC64;  
 CC Query Match 49.6%; Score 725; DB 1; Length 303;

Best Local similarity 51.2%; Pred. No. 9.7e-54;  
 Matches 145; Conservative 49; Mismatches 77; Indels 12; Gaps 3;  
 QY 5 ENSVDSKRIK NLEKTIHSESEMSDGSISLDS-----YKMPYEMGLCIITNNKMF 55  
 Db 19 EDSVDARKDRSSFPVSLSKRRKKNTMRSIKTRDRVPVQYNNMFEXIKGKIIINNKF 78  
 QY 56 HKSTGMTSGSDVAANLRETFRLKYEVRKNDLTREIYELMRDYSKEDHSRSSPV 115  
 Db 79 DKVYGMGRNTDADALFKCFPSLGGDYIYNDSCAKMODLLKKASEEDHTNACFA 138  
 QY 116 CYLLSHGEEGIIIFGTNGFVDLKKITNFGDRCRSITGCKPKLFIQACRGTELDGIEFD 175  
 Db 139 CILSHGEEVYIGKDGVTYPIKDLTAHFRGDRCKTLLEKPKLFQACRGTELDGIDQAD 198  
 QY 176 SGVDDNAC---HKIPVADLVASTAPGYISWRNSKDGSMFQISLCAMLKQYDKLEF 232  
 Db 199 SGPIINDTANPRKIVPEADLFVASTVPGYISWRNSPGRGSMFVQALCSLIEHKKDLEI 258  
 QY 233 MHILTRVNRKYATEFESFSPATFAKQICVSMILTKELF 275  
 Db 259 MQLTRVNDVRAHFEESODDPHFHEKQIPCVVSMILTKELF 301  
 RESULT 9  
 ICE6\_MOUSE STANDARD: PRT: 276 AA.  
 AC 008738;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Caspase-6 precursor (EC 3.4.22.-) (Apoptotic protease Mch-2).  
 GN CASP6.  
 OS Mus musculus (mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C3H/An;  
 RX MEDLINE=97190206; PubMed=9038361;  
 RA van de Craen M., Vandenaebelle P., Declercq W., van den Brande I.,  
 RA van Roo G., Molemans F., Schotte P., van Crielinge W., Beyaert R.,  
 RA Fiers W.;  
 RT "Characterization of seven murine caspase family members";  
 RL FEBS Lett. 403:61-69(1997).  
 CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES  
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES POLY(ADP-RIBOSE)  
 CC POLYMERASE IN VITRO, AS WELL AS LAMINS. OVEREXPRESSION PROMOTES  
 CC PROGRAMMED CELL DEATH (BY SIMILARITY).  
 CC -1- SUBUNIT: HETERODIMER OF A 18 kDa (P18) AND A 11 kDa (P11) SUBUNIT  
 CC (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, LIVER, KIDNEY,  
 CC TESTIS, AND HEART. LOWER LEVELS IN SPLEEN, SKELETAL MUSCLE, AND  
 CC BRAIN.  
 CC -1- PTM: CLEAVAGES BY CPP32, CASPASE-8 OR -10 GENERATE THE TWO ACTIVE  
 CC SUBUNITS (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.  
 CC -----  
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 CC -----  
 CC EMBL: Y13087; CAA73529.1; -  
 CC HSSP: P42574; IPAU.  
 CC MEROPS: C14.005; -  
 CC MGD: MGI:1312921; Casp6.  
 CC InterPro: IPR002398; ICE.



CC	-I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC	-----
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
CC	-----
DR	EMBL: Y12261; CAA72937.1; -
DR	EMBL: AE003771; AAF56939.1; -
DR	HSSP: P42574; IPAU.
DR	MEROPS: C14.015; -
DR	FLyBase: FBgn0019972; Ice.
DR	InterPro: IPR002398; ICE.
DR	InterPro: IPR002138; ICE_P10.
DR	InterPro: IPR001309; ICE_P20.
DR	PIfam: PF00655; ICE_P10; 1.
DR	PIfam: PF00656; ICE_P20; 1.
DR	PRINTS: PR00376; ILIHCENZYME.
DR	SMART: SM00115; CASc: 1.
DR	PROSITE: PS01122; CASPASE_CYS: 1.
DR	PROSITE: PS01121; CASPASE_HIS: 1.
DR	PROSITE: PS50207; CASPASE_P10; 1.
DR	PROSITE: PS50208; CASPASE_P20; 1.
FW	Hydrolase; Thiol protease; Zymogen; Apoptosis.
FT	PROPEP 1 28 BY SIMILARITY.
FT	CHAIN 29 217 CASPASE SUBUNIT P21 (BY SIMILARITY).
FT	PROPEP 218 230 BY SIMILARITY.
FT	CHAIN 231 339 CASPASE SUBUNIT P12 (BY SIMILARITY).
FT	ACT_SITE 169 169 BY SIMILARITY.
FT	ACT_SITE 211 211 BY SIMILARITY.
FT	CONFLICT 151 151 A -> S (IN REF. 1).
FT	CONFLICT 265 265 S -> T (IN REF. 1).
SO	SEQUENCE 339 AA; 37363 MW; E105ED29518507EC CRC64;
Query Match	34.3%; Score 502.5; DB 1; Length 339;
Best Local Similarity	39.2%; Pred. No. 5.3e-35;
Matches 111; Conservative 50; Mismatches 101; Indels 21; Gaps 6;	
QY	1 MENTENSVDSKSIKNLEPKII--HGSEMDSGISLDNSYKMDYPEMGLCTIINKNFKHS 58
DB	59 LANGSSPSSSSRYKRVAKMVTDRHAAE-----YNNRRKNNRMALJFNHEHEVP 107
QY	59 TGMSTSGTVDVDAANLKEPRNLKIEYRNKNDLTREIVELMRDYSKEDHSKSSFFCVL 118
DB	108 T-LKSRGTIVDCNLTIRVLKQIDFEYVYKDCRYKNDILRTIEVAASQNSHSDSDCLIVAI 166
QY	119 LSHGEGIIFFGTGPNVPLKKTINFFGRDRCRLTGKPKLFTIQAQRTETLDCGI-----E 173
DB	167 LSHHEMGYITAKDIOYKLDINWSTFNHNPRLSLAGKRLKLFITQACGDRLDGGVTLQRSO 226
QY	174 TDSGVDDDMACHKIPVADFLVAYSTAAGYYSWRNKSDGSMFTQISLAMLKQYADKLKLEFM 233
DB	227 TETDGDSSMS-YKIPVHADFLIAYSTVPGEYSWRNTRTGSWMFQISLAEALANGKRDLIL 285
QY	234 HILFRVNRKATPEEFESFDA-TFHAKQIPLCIYSMILTKLYF 275
DB	286 TLTFVCCQAVAVDFESCTPTPEMHQOKIPLITMLTRLIRF 328
RESULT 12	
ICEL_SPOFR	
ID ICEL_SPOFR	STANDARD; PRT; 299 AA.
AC P89116;	
DT 01-NOV-1997 (Rel. 35, Created)	
DT 01-NOV-1997 (Rel. 35, Last sequence update)	
DT 15-JUN-2002 (Rel. 41, Last annotation update)	
OS caspase-1 precursor (EC 3.4.22.-)	
DE Spodoptera frugiperda (Fall armyworm).	
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;	

OC Diptera: Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera.  
 OX NCBI\_TaxID=7108;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE=97153084; PubMed=899805;  
 RA Ahmed M., Srinivasula S.M., Wang L., Litwack G., Fernandes-Alnemri T., Alnemri E.S.;  
 RT "Spodoptera frugiperda caspase-1, a novel insect death protease that cleaves the nuclear immunophilin FKBP46, is the target of the baculovirus antiapoptotic protein p35.";  
 RL J. Biol. Chem. 272:1421-1424(1997).  
 CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES RESPONSIBLE FOR APOPTOSIS EXECUTION (BY SIMILARITY). INHIBITED BY THE BACULOVIRUS ANTI-APOPTOTIC PROTEIN P35. CLEAVES P35 AND NUCLEAR IMMUNOPHILIN FKBP46.  
 CC -1- SUBUNIT: HEPTAMER OF A 19/18 kDa (P19/18) AND A 12 kDa (P12) SUBUNIT.  
 CC -1- PTM: AN AUTOCATALYTIC MECHANISM GENERATES THE TWO ACTIVE SUBUNITS.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.  
 CC -----  
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 CC -----  
 DR EMBL: U81510; AAC7442.1; -  
 DR HSSP: PA2574; ICP3.  
 DR MEROPS: C14.015; -  
 DR InterPro: IPR002398; ICE.  
 DR InterPro: IPR002138; ICE\_P10.  
 DR InterPro: IPR001309; ICE\_P20.  
 DR Pfam: PF00655; ICE\_P10; 1.  
 DR Pfam: PF00656; ICE\_P20; 1.  
 DR SMART: SM00115; CASC; 1.  
 DR PROSITE: PS01122; CASPASE\_CYS; 1.  
 DR PROSITE: PS01121; CASPASE\_HIS; 1.  
 DR PROSITE: PS50207; CASPASE\_P10; 1.  
 DR PROSITE: PS50208; CASPASE\_P20; 1.  
 DR Hydroxylase; Thiol protease; Zymogen; Apoptosis.  
 FT PROPEP 1 28  
 FT CHAIN 29 184 CASPASE-1 SUBUNIT P19/18.  
 FT PROPEP 185 195 POTENTIAL.  
 FT CHAIN 196 299 CASPASE-1 SUBUNIT P12.  
 FT ACT\_SITE 136 136 BY SIMILARITY.  
 FT ACT\_SITE 178 178 BY SIMILARITY.  
 FT ACT\_SITE 178 178 BY SIMILARITY.  
 FT SEQUENCE 299 AA; 33527 MW; 99FAFED09B04EEDC CRC64;  
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 Query Match 32.1%; Score 470; DB 1; Length 299;  
 Best Local Similarity 40.5%; Pred. No. 2,4e-32;  
 Matches 100; Conservative 50; Mismatches 83; Indels 14; Gaps 5;

QY 37 YKNDYEMGLCIITINKNF--HKSTGMTSRGTVDVAANLRETFRNKLKYEVRNKNLDTRE 94  
 DB 53 YNNHNRHGMALIEHNEHDH---SLKSTGTINVDSDNLSKVLKLTGFEVTVFNNKSE 109  
 QY 95 EIVELEMDYKSKEDHRSRVVCLSHGEGIIITFNGPVYDLKKITNFFRGDCRSITGK 154  
 DB 110 EINKFIOQTAEHMDADCLVALVTHGELGMLYAKDTHYKPNMLWYTFADKCPITLAK 169  
 QY 155 PLKFIIOAGRTGELDGI-----ETDSQVDDDAKCKIPPEADPLAYATAPGYISRRNS 209  
 DB 170 PLKFIIOAGRTGELDGIILSTRTEDG---SPSTSYRIPIVHAPFLAFTVPQYFSKRRNT 226  
 QY 210 KDSWFIQSLCMLKQYADKLEFMHILTRVNRKVAATEFESFSD-ATFHAKKOIPICVSM 268  
 DB 227 TGSWMWQALCELRKRAGERDLITLITFYCQVALDFESNAPDSAMHQQKQVPCITSM 286  
 QY 269 LTRKELF 275  
 DB 287 LTRLLVF 293

RESULT 13  
 ID ICEL\_DROME  
 AC 002002; 09WIN0; STANDARD; PRT: 323 AA.  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Caspase-1 precursor (EC 3.4.22.-).  
 OS DCP-1 OR CG5370.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 216-248.  
 RC TISSUE=Embryo;  
 RX MEDLINE=97153052; PubMed=8999799;  
 RA Song Z., McCall K., Steller H.;  
 RT "DCP-1, a Drosophila cell death protease essential for development.";  
 RL Science 275:536-540(1997).  
 RN [2]  
 RP ERRATUM.  
 RA Song Z., McCall K., Steller H.;  
 RL Science 277:167-167(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkely;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amentides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Peiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abail J.F., Ashby A., An H.-J., Andrews-Frankoch C., Baldwin D.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos J., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Doudson K., Doup L.E., Donnes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegyam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheele F., Shen H.,  
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Silver E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley R.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES RESPONSIBLE FOR APOPTOSIS EXECUTION (BY SIMILARITY).  
 CC PROBABLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP). LOSS OF ZYGOTIC DCP-1 FUNCTION CAUSES LARVAL LETHALITY AND MELANOTIC



RA Medema J.P., Scaffidi C., Kischkel F.C., Shevchenko A., Mann M.,  
 RA Kramer P.H., Peter M.E.,  
 RT "FLICE is activated by association with the CD95 death-inducing  
 RT signaling complex (DISC)."  
 RL EMBL J. 16:2794-2804(1997).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS):  
 RX MEDLINE:99451259; PubMed:10508784;  
 RA Blanchard H., Kodandapani L., Mittle P.R.E., Di Marco S., Krebs J.F.,  
 RA Wu J.C., Tomaselli K.J., Grutter M.G.;  
 RT "The three-dimensional structure of caspase-8: an initiator enzyme in  
 RT apoptosis."  
 RL Structure 7:1125-1133(1999).  
 CC -1- FUNCTION: MOST UPSTREAM PROTEASE OF THE ACTIVATION CASCADE OF  
 CC CASPASES RESPONSIBLE FOR THE FAS-RECEPTOR MEDIATED (CD95) AND  
 CC TNF-R1 INDUCED CELL DEATH. BINDING TO THE ADAPTOR MOLECULE FADD  
 CC RECRUITS IT TO EITHER RECEPTORS. THE RESULTING AGGREGATE CALLED  
 CC THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS FLICE/MACH  
 CC PROTEOLYTIC ACTIVATION. THE ACTIVE DIMERIC ENZYME IS THEN  
 CC LIBERATED FROM THE DISC AND FREE TO ACTIVATE DOWNSTREAM APOPTOTIC  
 CC PROTEASES. PROTEOLYTIC FRAGMENTS OF THE N-TERMINAL PROPEPTIDE  
 CC (TERMED CAP3, CAP5 AND CAP6) ARE LIKELY RETAINED IN THE DISC.  
 CC CLEAVES AND ACTIVATES CASPASE-3, -4, -6, -7, -9, AND -10. MAY  
 CC PARTICIPATE IN THE GRANZYME B APOPTOTIC PATHWAYS. PROTEOLYTICALLY  
 CC CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP). HYDROLYZES THE SMALL-  
 CC MOLECULE SUBSTRATE, AC-ASP-GLU-VAL-ASP-1-AMC. LIKELY TARGET FOR  
 CC THE COMPLEX VIRUS CRMA DEATH INHIBITORY PROTEIN.  
 CC -1- SUBUNIT: HETERODIMER OF A 18 kDa (P18) AND A 10 kDa (P10) SUBUNIT.  
 CC INTERACTS WITH CFLAR.  
 CC -1- ALTERNATIVE PRODUCTS: 8 ISOFORMS: 1-ALPHA (SHOWN HERE), 2-  
 CC ALPHA/MCH5-BETA, 3-ALPHA, 4-ALPHA, 1-BETA, 2-BETA, 3-BETA AND 4-  
 CC BETA. ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: ALPHA 1 AND BETA 1 ISOFORMS ARE EXPRESSED IN A  
 CC WIDE VARIETY OF TISSUES. HIGHEST EXPRESSION IN PERIPHERAL BLOOD  
 CC LEUCOCYTES, SPLEEN, THYMUS, AND LIVER. BARELY DETECTABLE IN BRAIN,  
 CC TESTIS, AND SKELETAL MUSCLE.  
 CC -1- PTM: GENERATION OF THE SUBUNITS REQUIRES ASSOCIATION WITH THE  
 CC DISC. WHEREAS ADDITIONAL PROCESSING IS LIKELY DUE TO THE  
 CC AUTOCATALYTIC ACTIVITY OF THE ACTIVATED PROTEASE. GRANZYME B AND  
 CC CASPASE-10 CAN BE INVOLVED IN THESE PROCESSING EVENTS.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.  
 CC -1- SIMILARITY: CONTAINS 2 DEATH EFFECTOR DOMAINS (DED).  
 CC  
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 CC  
 DR EMBL: X98172; CA66853.1; -  
 DR EMBL: X98173; CA66854.1; -  
 DR EMBL: X98174; CA66855.1; -  
 DR EMBL: X98175; CA66856.1; -  
 DR EMBL: X98176; CA66857.1; -  
 DR EMBL: X98177; CA66858.1; -  
 DR EMBL: X98178; CA66859.1; -  
 DR EMBL: U58143; AAC50602.1; -  
 DR EMBL: U60520; AAC50645.1; -  
 DR EMBL: AF102146; AAD24962.1; -  
 DR EMBL: AF102139; AAD24962.1; JOINED.  
 DR EMBL: AF102140; AAD24962.1; JOINED.  
 DR EMBL: AF102141; AAD24962.1; JOINED.  
 DR EMBL: AF102142; AAD24962.1; JOINED.  
 DR EMBL: AF102143; AAD24962.1; JOINED.  
 DR EMBL: AF102144; AAD24962.1; JOINED.  
 DR EMBL: AF102145; AAD24962.1; JOINED.  
 DR EMBL: AF009620; AAB70913.1; -  
 DR PDB: 1ODU; 10-JUL-00.  
 DR MEROPS; C14.009; -  
 DR Genem; HGNC:1509; CASP8.  
 DR MIM; 601763; -

DR InterPro: IPR001875; DED.  
 DR InterPro: IPR002138; ICE\_p10.  
 DR InterPro: IPR001309; ICE\_p20.  
 DR Pfam: PF00655; ICE\_p10; 1.  
 DR Pfam: PF00656; ICE\_p20; 1.  
 DR Pfam: PF01335; DED; 2.  
 DR PROSITE: PS01122; CASPASE\_CYS; 1.  
 DR PROSITE: PS01121; CASPASE\_HIS; 1.  
 DR PROSITE: PS0207; CASPASE\_P10; 1.  
 DR PROSITE: PS0208; CASPASE\_P20; 1.  
 DR PROSITE: PS0168; DED; 2.  
 KW Hydrolase; Thiol protease; Apoptosis; Zymogen; Alternative splicing;  
 KW Repeat; 3D-structure.  
 FT PROPEP 1 216  
 FT CHAIN 217 374  
 FT PROPEP 375 384  
 FT CHAIN 385 479  
 FT ACT\_SITE 317 317  
 FT ACT\_SITE 360 360  
 FT DOMAIN 2 80  
 FT VARSPLIC 100 177  
 FT VARSPLIC 102 102  
 FT VARSPLIC 184 198  
 FT VARSPLIC 184 220  
 FT VARSPLIC 184 267  
 FT VARSPLIC 199 235  
 FT VARSPLIC 221 479  
 FT VARSPLIC 236 479  
 FT VARSPLIC 269 276  
 FT VARSPLIC 277 479  
 FT CONFLICT 285 285  
 FT CONFLICT 294 294  
 FT CONFLICT 331 331  
 SO SEQUENCE 479 AA; 55391 MW; 7A5FEAA6B39B582F CRC64;  
 Query March 28.8%; Score 421; DB 1; Length 479;  
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 Matches 102; Conservative 49; Mismatches 91; Indels 28; Gaps 8;  
 QY 24 SESMDSGISLDSNYKMDPEMGLCIITNNKFNHST-----GMTSRSGTVDANLRE 76  
 DB 217 SESQ---TLDKVYQMKSKPRGVCILINNNHFAKAREKVPKLHSIRDRGTHLDAGALT 272  
 QY 77 TFRNLKTYVRKNNDITREIYELMDVSKEDSKSSFPVCULLSHGEEIITGTNG-PVD 135  
 DB 273 TFEELHFEIKPHDDCTVQIYEILKLYQIMDSNMDCFLSHGDKIIVGTQDEAP 332  
 QY 136 LKLTNFRGDRCSRLTGKPKFLITQACRGTELDGI--ETDSG---VDDMACHK--- 186  
 DB 333 IYELTSQFTGLKPSLAKPKVFTIQCAGDNYQKGIPEYETSEDPYLEMDLSSQOTRY 392  
 QY 187 IPVEADFLYASTAPGYYSWRNSKDGSMFTIOSLCAMLKQYADK-LEFMHILRVNRKVA 245  
 DB 393 IPDEADFLGMATVNCVSYRNPAEGTWIOSLQSLRRRCRGDDILITLEVNEVEVN 452  
 QY 246 EFESRSPDATHAKQIPCIYSMLTKELVF 275  
 DB 453 K-----DCKRMGRKMPQPTFTLKKLVF 476  
 RESULT 15  
 ID ICE9\_HUMAN STANDARD; PRT; 416 AA.  
 AC P55211; O92852; O95348; Q9UIJ8; Q9UEQ3;  
 DT 01-OCT-1996 (Rel. 34, Created)



DT 16-OCN-2001 (Rel. 40, last sequence update)  
DT 15-JUN-2002 (Rel. 41, last annotation update)  
DE Caspase-9 precursor (EC 3.4.22.-) (CASP-9) (ICE-like apoptotic  
DE protease 6) (ICE-LAP6) (Apoptotic protease Mch-6) (Apoptotic protease  
DE activating factor 3) (APAF-3).  
GN CASP9 OR MCH6.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI:TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96279246; PubMed=8662294;  
RA Duan H., Orth K., Chinnaiyan A.M., Poirier G.G., Froelich C.J.,  
RA He W., Dixit V.M.;  
RT "ICE-LAP6, a novel member of the ICE/Ced-3 gene family, is activated  
RT by the cytotoxic T cell protease granzyme B.";  
RL J. Biol. Chem. 271:16720-16724(1996).  
RN [2]  
RP SEQUENCE FROM N.A., AND PROCESSING.  
RC TISSUE-T-cell;  
RX MEDLINE=97059171; PubMed=8900201;  
RA Srinivasula S.M., Fernandes-Alnemri T., Zangrilli J., Robertson N.,  
RA Armstrong R.C., Wang L., Trepant J.A., Tomaselli K.J., Litwack G.,  
RA Alnemri E.S.;  
RT "The Ced-3/interleukin beta converting enzyme-like homolog Mch6 and  
RT the lamin-cleaving enzyme Mch2alpha are substrates for the apoptotic  
RT mediator CPP32.";  
RL J. Biol. Chem. 271:27099-27106(1996).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99315341; PubMed=10384055;  
RA Hadam S., Nasir J., Nichol K., Rasper D.M., Vallancourt J.P.,  
RA Shera S.W., Beatty B.G., Ikeda J.E., Nicholson D.W., Hayden M.R.;  
RT "Genomic organization of the human caspase-9 gene on chromosome  
RT 1p36.1-p36.3.";  
RL Mamm. Genome 10:757-760(1999).  
RN [4]  
RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
RX MEDLINE=99168502; PubMed=10070954;  
RA Srinivasula S.M., Ahmad M., Guo Y., Zhan Y., Lazebnik Y.,  
RA Fernandes-Alnemri T., Alnemri E.S.;  
RT "Identification of an endogenous dominant-negative short isoform of  
RT caspase-9 that can regulate apoptosis.";  
RL Cancer Res. 59:999-1002(1999).  
RN [5]  
RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
RC TISSUE-Stomach cancer;  
RX Izawa M., Mori T., Ito H., Saitenji T.;  
RA "Molecular cloning and sequencing of a cDNA predicting an alternative  
RA form of pro-caspase-9 from human gastric cancer cell lines.";  
RT Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
RX Mino Y., Komori T., Fujita E.;  
RA "A novel splicing product of human caspase-9 lacking protease  
RA activity.";  
RT Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
RX MEDLINE=99107856; PubMed=9890966;  
RA Seol D.W., Billiar T.R.;  
RT "A caspase-9 variant missing the catalytic site is an endogenous  
RT inhibitor of apoptosis.";  
RL J. Biol. Chem. 274:2072-2076(1999).  
RN [8]  
RP FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES  
RP RESPONSIBLE FOR APOPTOSIS EXECUTION. BINDING OF CASPASE-9 TO APAF-  
RA 1 LEADS TO ACTIVATION OF THE PROTEASE WHICH THEN CLEAVES AND  
CC ACTIVATES CASPASE-3. PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE)  
CC POLYMERASE (PARP).  
CC -I- FUNCTION: THE SHORT ISOFORM LACKS ACTIVITY IS AN DOMINANT-NEGATIVE  
CC INHIBITOR OF CASPASE-9.  
CC -I- SUBUNIT: Heterodimer of a 35 kDa (P35) and a 10 kDa (P10) subunit.

CC Caspase-9 and APAF1 bind to each other via their respective NH2-  
CC terminal CED-3 homologous domains in the presence of cytochrome C  
CC and ATP. Interacts with BIRC7  
CC -I- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG/9L/ALPHA FORM (SHOWN  
CC HERE) AND A SHORT/9S/BETA FORM; ARE PRODUCED BY ALTERNATIVE  
CC SPLICING.  
CC -I- TISSUE SPECIFICITY: UBIQUITOUS, WITH HIGHEST EXPRESSION IN THE  
CC HEART, MODERATE EXPRESSION IN LIVER, SKELETAL MUSCLE, AND  
CC PANCREAS. LOW LEVELS IN ALL OTHER TISSUES.  
CC -I- PTM: CLEAVAGES AT ASP-315 BY GRANZYME B AND AT ASP-330 BY CPP32  
CC INVOLVED IN THESE PROCESSING EVENTS.  
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.  
CC -I- SIMILARITY: CONTAINS 1 CARD DOMAIN.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; U56390; AAC50640.1; -;  
CC EMBL; U60521; AAC50776.1; -;  
CC EMBL; AB019205; BAA82697.1; -;  
CC EMBL; AB019197; BAA82697.1; JOINED.  
CC EMBL; AB019198; BAA82697.1; JOINED.  
CC EMBL; AB019199; BAA82697.1; JOINED.  
CC EMBL; AB019200; BAA82697.1; JOINED.  
CC EMBL; AB019201; BAA82697.1; JOINED.  
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CC EMBL; AB019203; BAA82697.1; JOINED.  
CC EMBL; AB019204; BAA82697.1; JOINED.  
CC EMBL; AF093130; AAD12248.1; -;  
CC EMBL; AB015653; BAA78780.1; -;  
CC EMBL; AB020979; BAA787905.1; -;  
CC EMBL; AF110376; AAD13615.1; -;  
CC HSP: P42574; 1PAU.  
CC MEROPS; C14.010; -;  
CC Genew; HGNC:1511; CASP9.  
CC MIM; 602234; -;  
CC InterPro; IPR001315; CARD.  
CC InterPro; IPR002398; ICE.  
CC InterPro; IPR002138; ICE\_P10.  
CC InterPro; IPR001309; ICE\_P20.  
CC Pfam; PF00619; CARD; 1.  
CC Pfam; PF00655; ICE\_P10; 1.  
CC Pfam; PF00656; ICE\_P20; 1.  
CC PRINTS; PR00376; TL1BCENZME.  
CC SMART; SM00114; CARD; 1.  
CC SMART; SM00115; CASC; 1.  
CC PROSITE; PSS0209; CARD; 1.  
CC PROSITE; PSS0122; CASPASE\_CYS; 1.  
CC PROSITE; PSS01121; CASPASE\_HIS; 1.  
CC PROSITE; PSS0207; CASPASE\_P10; 1.  
CC PROSITE; PSS0208; CASPASE\_P20; 1.  
CC Hydrolase; Thiol protease; zymogen; Apoptosis; Alternative splicing.  
CC POTENTIAL.  
CC CASPASE-9 SUBUNIT P35.  
CC CASPASE-9 SUBUNIT P10.  
CC CARD.  
CC BY SIMILARITY.  
CC MISSING (IN SHORT ISOFORM).  
CC A -> V (IN REF. 1 AND 7).  
CC S -> R (IN REF. 1, 4, 5 AND 7).  
CC A -> G (IN REF. 1).  
CC P -> L (IN REF. 1).  
CC O -> R (IN REF. 1).  
CC SEQUENCE 416 AA; 46195 MM; 874B90F17F8DC4CD CRC64;

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Query Match          28.0%; Score 410; DB 1; Length 416;
Best Local Similarity 32.8%; Pred. No. 4e-27;
Matches 90; Conservative 51; Mismatches 91; Indels 42; Gaps 4;

QY 34 DNSYKMDYPMGICIIINKNFKHSTGMSRSGETVDANLRETFRNLYEVRNKNDLTR 93
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Db 150 DLAYILSMERPCGHCLINNNVFCRESGLRTRTGSINIDCEKLRFRSSPHFWEVKGDLT 209
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 94 EEIVELMRDYSKEDHGRSSFCVLLSHGEE-----GIIFGTNG-PVDLKTITNFERG 145
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 210 KKNVLALELDAQDGHALDCCVVVILSHGQASHLOFPGAVGTGCGPVSVEKIVNIENG 269
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 146 DRCRSLTGKPKLFIIOACRGTETELDCGIETDSGYDDDM----- 182
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 270 TSCPSLGGKPKLEFIQACGGEQKDHGEVASTSPEDSPGSNPEPDATPFOEGLTRFDQL 329
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 183 -ACHKIPVADFLYAYSTAGYYSWRNSKDGSMFIOSLCAMLKQYADKLEFMHILTRVNR 241
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 330 DAISSLPTPSDIFVSYSTPFGFVSWRDPKSGSMVETLDDIFEQMAHSEDLQSLLRVAN 389
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 242 KYATEFESESFDAITFAKKOIPCIIVSMILTKELIF 275
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 390 AVSVK-----GIYKQMPGCFNPLRKKLFF 413
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 Job time : 10.5517 secs